STIC-Biotech/ChemLib

166285

From:

Dunston, Jennifer

Sent:

Tuesday, September 20, 2005 11:49 AM

To:

STIC-Biotech/ChemLib

Subject:

Sequence Search 10/705757

Please do a sequence search for SEQ ID NOS: 1, 3 and 5 against the commercial protein databases. SEQ ID NOS: 1, 3 and 5 are 2623, 1302 and 942 nt in length, respectively.

Thank you.

Jennifer Dunston, Ph.D. USPTO Art Unit 1636 REM 2B76 Mailbox: REM 2C70 (571) 272-2916

Searcher:
Searcher Phone:
Date Searcher Picked up:
Date completed:
Searcher Prep Time:
Online Time:

Type of Search
NA# AA#:
S/L: Oligomer:
Encode/Transl:
Structure #: Text:
Inventor: Litigation:

Vendors and cost where applicable
STN:_____
DIALOG:___
QUESTEL/ORBIT:____
LEXIS/NEXIS:___
SEQUENCE SYSTEM:____
WWW/Internet:____
Other (Specify):_____

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Command line parameters:

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-LOOPEXT=0 -UNITS=51ts -START=1 -END=1 -MARTIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-644-450-9
US-08-461-30818-26
US-08-461-379A-26
US-08-463-0748-26
US-08-463-0748-26
US-08-465-85C-26
US-08-652-446-26
US-09-237-543-8
US-09-237-543-7
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Sequence 18441, A	equence 4, Appl	equence 2, Appl	equence 2, Appl	equence	equence 4, Appl	e 10, App	e 32, Ap	9 7418,	9 7417,	6	2,	4.	Ņ		2	Sequence 2, Appli	œ '		11,	11, App	38,	Ņ	Sequence 7140, Ap	e 4, Appl	4.	e 6, Appl	equence 6,	equence 2, Appl	e 2, Appl	5, Appl	Sequence 5, Appli	e 41, App

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                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: MOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
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Sequence 9, Application US/09644450
PARCENT NO. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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        CCTTTCGAGCATGACGAGAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT
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Sequence 26, Application US/08463081B

Patent No. 5871960

Patent No. 5871960 5837487

GENERAL INFORMATION:

MPPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5 Poly TITLE OF INVENTION: Vector and Transformed Cell The NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI STREET: 444 South Flower St. - Suite 1900

CITY: Los Angeles

STATE: California
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Best Local Similarity:
Query Match:
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FILING DATE: 5-7UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-193
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38150 (DART-060)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 90071
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN REJEASE #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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TOPOLOGY: n.a.
MOLECULE TYPE: peptic
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                               Sequence 26, Application US/08461379A

Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                          ADDRESSEB:
CITY: Vall
STATE: Pen
                                                ZIP:
                                                            COUNTRY:
                                                                                                                    ADDRESSEE: Ratner & Prestia
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Best Local Similarity:
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US-08-461-379A-26
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APPLICATION NUMBER: USSN 08/330,108; 08/104,736
APPLICATION NUMBER: & 07/796,066

FILING DATE: 27-0CT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: 30,930

REFERENCE/DOCKET NUMBER: 30,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610,470-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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SOFTWARE: Patentin Releas
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 5-JUNE-1995
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RESULT 5
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US-08-462-390B-26
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                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-CCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 0,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Smith,
                                                                                TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
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ADDRESSEE: (B) STI
CITY: Valley Forge
                               STRANDEDNESS: n.a. TOPOLOGY: n.a.
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                                                                                  313 amino acids
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Pred. No.:
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                                                    TTCGAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCT 1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 313 amino acids
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                                                                                                                                                                                                                                                                                                                                                          TYPE: peptide STRANDEDNESS: n.a. TOPOLOGY: n.a.
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. (B) STREET:
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Matches:
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COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6
TITLE OF INVENTION: Transformed Cell Thereof,
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                ADDRESSEE: .
CITY: Los Angeles
STATE: California
                                                                                           COUNTRY: USA
ZIP: 900071
                                                                                                                                       ADDRESSEE: PRETTY, SCHROEDER & PC
ADDRESSEE: . (B) STREET:
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APPLICATION NUMBER: USSN 08/33
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/10
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/75
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 3
REFERENCE/DOCKET NUMBER: P66 3
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 622-7700
TELEPAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENUTH: 31 amino 2cids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: peptide STRANDEDNESS: n TOPOLOGY: n.a. MOLECULE TYPE: pe
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               GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp
                         GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC
                                                         GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn
                                                                                                                               GAGGAGCTGGCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAAC
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1657.00
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Gaps:
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Matches:
Conservative:
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RESULT 8
US-08-652-446-26
### Sequence 26, Ap.
### Patent No. 6657
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FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,390
PRILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,390
PRIOR APPLICATION NUMBER: 08/462,390
PRIOR APPLICATION NUMBER: 08/462,390
PRIOR APPLICATION NUMBER: 08/465,585
PRIOR APPLICATION NUMBER: 08/465,585
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 5-JUN-1:
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STATE: California
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(B) STREET:
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Query Match:
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; STRANDEDNESS: n.a.
; TOPOLOGY: n.a.
; MOLECULE TYPE: peptide
US-08-652-446-26
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APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 7966 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (213) 622-77
TELEPAX: (213) 489-4210
INFORMATION FOR SEQ ID NO:
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LENGTH: 313 amino acid
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                                  GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp
                                                    GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC
                                                                                                                                          TGCGGGGTGCTACACCGCGACATCAAGGACGAAAAACATCCTTATCGACCTCAATCGCGGC
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Matches:
Conservative:
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Sequence 8, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:

APPLICANT: Kapeller, Rosana

ITILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT PILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 313

TYPE: PRT

ORGANISM: Rattus norvegicus
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                                                                AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG
                                                                                            GGCCCGCTACTGGGCAGCGGCGCTTCGGCTCGGTCTACTCAGGCATCCGCGTCTCCGAC
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TCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTG
                 ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe
                                     CCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGTTTC
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                                                       AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu
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TYPE: PRT
ORGANISM: Rattus
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Percent Similarity:
Best Local Similarity:
Query Match:
                                US-10-705-757-1 (1-2623) x US-09-644-450-8 (1-313)
                                                                                                                                                                                                                                                                     Sequence 8, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 200-08-23
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 89
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RESULT 11

US-09-237-543-7

¡ Sequence 7, Application US/09237543A

¡ Patent No. 6143540

¡ GENERAL INFORMATION:

¡ APPLICANT: Kapeller, Rosana

¡ TITLE OF INVENTION: NOVEL MOLECULES OF THE HK

¡ TITLE OF INVENTION: AND USES THEREOF

¡ FILE REFERENCE: 035800/175631

¡ CURRENT APPLICATION NUMBER: US/09/237,543A
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NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
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RESULT 12
US-09-644-450-7
; Sequence 7, Application US/09644450
; Patent No. 6383791
; GENERAL INFORMATION:
; APPLICANT: Kapeller, ROSANA
; TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 313
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; ORGANISM: Mus musculus
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US-07-857-224B-41
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
CLASSIFICATION: 436
PRIONE: (International) 41 1 632 2830
TELEPAX: (International) 41 1 632 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 41, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                  TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Benner, TITLE OF INVENTION:
                                                   FEATURE: Protein kinase PUBLICATION INFORMATION:
                                                                                                                                        TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                        ORIGINAL SOURCE:
 AUTHORS:
AUTHORS:
AUTHORS:
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STATE: none
                                                                                    ORGANISM:
                                                                                                                      DESCRIPTION:
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                                                                      Protein kinase; Table 8 Column
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; AUTHORS: Hunter, T.
; TITLE: The protein kinase f;
; JOURNAL: Science
; VOLUME: 241
; VOLUME: 241
; PAGES: 42-52
; DATE: 1998
US-07-857-2248-41
 RESULT 14
US-09-237-543-5
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; TYPE: PRT
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US-09-237-543-5
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GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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TGCTCTTGTCCAAAATCAACTCGCCTTGCCCACCTGCGCGCCGCCGCCC-----TGCAACG
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etLeuLeuSerLysPheGlySerLeuAlaHisLeu---CysGlyProGlyGlyValAspH
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	-10-705-757-1 43 C	24.00% Indels: 3 Gaps:	Alignment Scores: Pred. No.: 1149.50 Score: 1149.50 Matches: Percent Similarity: 66.59% Conservative: 37	; ORGANISM: Rattue norvegicue US-09-644-450-5	; SOPTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 5 ; LENGTH: 455	FILE REFERENCE: 035800/175631 ; FILE REFERENCE: 035800/175631 ; CURRENT APPLICATION NUMBER: US/09/644,450 ; CURRENT FILING DATE: 2000-08-23 . NUMBER OF SEO ID NOS. 11	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Kapeller, Rosana TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY TITLE OF INVENTION: AND HERS THEREOF	RESULT 15 US-09-644-450-5 ; Sequence 5, Application US/09644450 . Parent No. 618791	Oy 1177 CAGATAGGCCAACCTTCGAAGAAATCCAGAACGATCCATGGATG 1220 :::	Qy 1117 GGCAGAGGGTCTCTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGGCCCTGAGACCAT 1176 :::	Qy 1057 TGTGTGGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCA 1116	Qy 997 ATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGG 1056	Qy 937 CCGTCTACACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACC 996	Qy 877 ACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGGTCGGGGGGCGCTGCTCAAGGACA 936	Oy 817 GGCACTGCCACAACTGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCG 876	Oy 757 GGGGAGCCCTGCAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGC 816	Qy 697 TCGTCCTGATCCTGGAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAA 756 ::: :::
Q Q	Db Qy	B Q	B &	B &	D Q	Db Oy	D Qy	Qy dd	B 성	p Q	Db Qy	D Qy	p Q	Qy dd	D Q	D Q	Db Qy
1117 GGCAGAGGGTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCAT 1176 :::	TGTGTGAGATATTCCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCA 1	997 ATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCTGGGGGATCCTGCTGTATGATATGG 1056	937 CCGTCTACACGGACTTCGATGGGACCCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACC 996 	877 ACCTCAATCGCGGCGAGCTCAAGCTCATCGACTTCGGGTCGGGGGGCCTGCTCAAGGACA 936 	817 GGCACTGCCACAACTGCGGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCG 876	757 GGGGAGCCCTGCAAGAGGAGCTGGCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGC 816 	697 TCGTCCTGATCCTGGAGAGGCCCGAGAGCCGGTGCAAGATCTCCTTCGACTTCATCACGGAAA 756 ::: :::	639AGCTCGGGTTTCTCCGGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTT 696 ::	583 GAGAGCTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTG 638 	523 TCTCCGACAACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGG 582 ::::: ::	463 ACCAGGTGGGCCGCTACTGGGCAGCGGCGGCTTCGGCTCCGGTCTACTCAGGCATCCGCG 522	406 ACCTGCACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGT 462 	352 TGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCCCTGCAACG 405 	292 GCTCCGGCTCCTGCGCAGCTCCTCTGGCACGTCCCTGCGCCGACATTCTGGAGGTTGGA 351	232 CAGCCGCACGCACCGCAGCACAGCACAGCCCCAGGCATAGCTTCGGCACAGCCCCG 291	172 CAGTCCCGGCAGCGCCTCAGTTGTCCTCCGACTCGCCCTCGGCCTTCGCGCAGCGCAGCA 231 :: 114 erValProAspGlySerGlu	148 ACCCCGCTGGC

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Result
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-MODEL-frame+ n2p, model - DEV=xlp
-Q=/Ggn2_1/USPTO_spool_p/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-Q=/Ggn2_1/USPTO_spool_p/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blts -START-1 -ENUD-1 -MATRIX=blosum62 -TRANS=human40.cdi -LICT=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=pto -NORM=cxt -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USER=US10705757 GGCN_1_1_256 GWTUNET_22092005_115015_22141 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -KGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Maximum DB seq length: 200000000
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 1636
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2: pir2:
3: pir3:
4: pir4:
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Fgapop 6.0 , F
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ALIGNMENTS

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A; Molecule type: mRNA A; Residues: 1-14, 'RA', 'I7-313 <ZAK> A; Cross-references: GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:g189957 A; Cross-references: GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:g189957 R; Domen, J.; Von Lindern, M.; Hermans, A.; Breuer, M.; Grosveld, G.; Berns, Oncogene Res. 1, 103-112, 1987 A; Molecule type: mRNA
A; Residues: 1-313 < MSE>
A; Residues: 1-313 < MSE>
A; Residues: 1-313 < MSE>
A; Cross-references: GB: M24779; NID: g1066790; PIDN: AAA81553.1; PID: g1066791
A; Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
Gene 54, 105-111, 1987
A; Title: The cDNA sequence and gene analysis of the human pim oncogene.
A; Reference number: A27476; MUID: 87277423; PMID: 3475233
A; Accession: A27476 A;Crobs-references: UNIPROT:P11309; GB:M27903; NID:g189958; PIDN:AAA60090.1; PID:g38702. R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M. J. Cell. Blochem. 35, 105-112, 1987 J. Cell. Blochem. 35, 105-112, 1987 A;Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene rela. A;Reference number: A46554; MUID:88115604; PMID:3429489 C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JU0327; A46554; A27476; I58412
R;Reeves, R: Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human oncogene, pim-1.
A;Reference number: JU0327; MUID:90382681; PMID:2205533
A;Accession: JU0327 A;Title: Comparison of the human and mouse PIM-1 cDNAs: A;Reference number: I58412; MUID:88217305; PMID:3329709 A;Accession: I58412 A;Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-313 < REE> protein kinase (EC 2.7.1.37) pim-1 - human N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene A; Accession: A46554 type: mRNA Nucleotide sequence and immunolo

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A;Residues: 1-313 <DOM>
A;Cross-references: GB:M54915; NID:g189961; PIDN:AAA36447.1; PID:g189962
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;denetics:
A;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoning;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;36-290/Domain: protein kinase homology <KIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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                                                                                                   GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC
                                                                                                                                     CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly
                                                                                                                                                TGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGC
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          AGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATT
                                                                                                                                                                                 GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn
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RESULT 2

protein kinase (EC 2.7.1.37) pim-1 - rat

protein kinase (EC 2.7.1.37) pim-1 - rat

protein kinase (EC 2.7.1.37) pim-1 - rat

N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene prote

C;Becies: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004

C;Accession: S26298

R;Wingett, D.; Reeves, R.; Magnuson, N.S.

Nucleic Acids Res. 20, 3183-3189, 1992

A;Title: Characterization of the testes-specific pim-1 transcript in rat.
A;Reference number: S26298; MUID:92319852; PMID:1620615

A;Accession: S26298

A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; EMBL:X63675; NID:g56902; PIDN:CAA45214.1; PID:g56903

A;Residues: 1-313 <WIN>
A;Residues: 1-313 <WIN>
A;Residues: 1-313 <WIN>
A;Residues: 1-313 <WIN>
A;Rote: testis-specific transcript is shorter and more stable than the somatic transcript; Note: testis-specific transcript is shorter and more stable than the somatic transcript; Pinction:
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Reywords: AIT; autophosphorylation; phosphortein; protein kinase homology
C;Reywords: AIT; autophosphorylation; phosphortein; phosphotransferase; proto-oncogene
F;667/Active site: Lys #status predicted

F;67/Active site: Lys #status predicted
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Best Local Similarity:
AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG
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RESULT 3

TVMSP1

protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_ch
C;Accession: A24169
R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, 1
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; N:
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Superfamily: kinase-related transforming protein; protein
A;Description: catalyzes the formation of peptidyl-serine-pl
C;Superfamily: kinase-related transforming protein; protein
C;Keywords: ATP; autophosphorylation; bhosphotransferase; p:
F;36-239/Domain: protein kinase homology <XIN>
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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                Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni; buperfamily: kinase-related transforming protein; protein kinase homology; keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; serine/threon; 26-290/Domain: protein kinase homology «KIN»; 44-52/Region: protein kinase ATP-binding motif; 44-52/Region: protein kinase ATP-binding motif
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                                                                                                                                    NID:g200352;
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                    GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA
                                                           TTCGAAGAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCT
                                                                                                    TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC
                                                                                                                                   ProPheGluHisAspGluGluIleIleLysGlyGlnValPhePheArgGlnThrValSer
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         eHisLeuHisSerLeuSerProGlySerSerLys
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A;Cross-references: GB:L41495;
A;Note: 37K form
A;Accession: R43000
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C;Comment: Pim-2 autophosphorylates at unknown sites.
C;Genmetne: Bim-2
A;Genetics:
A;Gene: Pim-2
A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG
A;Note: locus between A-raf and Act-7, near Kv4.1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin C;Superfamily: kinase-related transforming protein, protein kinase homology
C;Superfamily: kinase-related transforming brotein, protein kinase homology
C;Keywords: alternative initiators; ATP; autophosphorylation; phosphoprotein; phosphotra
F;89-345/Domain: protein kinase ATP-binding motif
F;120/Active site: Lys #status predicted
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C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
C;Date: 10-Oct-1995 #sequence revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: S55333; A43093; B43093
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Guld
R;van der Lugt, N.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Guld
EMBO J. 14, 2536-2544, 1995
A;Title: Proviral tagging in E-mu-myc transgenic mice lacking the Pim-1 pro
A;Reference number: S55333; MUID:95300786; PMID:7781606
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A;Molecule type: mRNA
A;Residues: 'M',61-370 <VA3>
A;Cross-references: GB:L41495;
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A; Residues: 'M', 27-370
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                        ArgAlaAlaPheGluAlaGluTyrArgLeuGlyProLeuLeuGlyLysGlyGlyPheGly
                                                         AAGGAGCCCCTGGAGTCGCAGTACCAGGTGGGCCCCCCTACTGGGCAGCGGCGGCTTCGGC
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A;Reference number: Z19538
A;Recession: T22255
A;Status: preliminary; translated from A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; ENA
A;Experimental source: clone F45H7
C;Genetics:
A;Gene: CESP:F45H7.4
                                                                                                                                                                                                hypothetical protein F45H7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T22255

R;Percy, C.
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ThrValPheAlaGlyHisArgValThrAspArgArgGinValAlaIleLysValIleSer
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A;Introns: 72/3; 160/3; 310/1
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   GlyProLeuProPhePheValProValSerAlaGluValLy8AspLeuIleSerLy8Cy8
                                                                                                                                                                                                   GGCCAGGITTTCTTCAGGCAGAGGGTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGC
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                            GAAACTGCTGAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAATAGCAGCCTTTC
                                                                                        CAAGATGTTCTCCTG------CCCCAG
                                                                                                                                               GTGCGGCACTGCCACAACTGCGGGGTGCTACACCGCGACATCAAGGACGAAAAACATCCTT
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                                                         LysGlnGlnThrLeuSerTrpAspAlaLeuThrLysAsnLysValGlnLysLysThrSer
                                                                                                                  LysCysSerLys---ValArgGlyValIleArgLeuLeuAspTrpTyrSerIleProGlu
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hypothetical protein C06E8.3 - Ca
C;Species: Caenorhabditis elegans
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A;Introns: 24/1; 76/3;
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                                            serLysHisGlyLeuLeuHisArgAspIleLysAspGluAsnLeuIleValAsnMetAsn
                                                                                                    AsnGluAspMetGlyLysPheIlePheLysGlnValIleThrThrValPheAsnMetTyr
                                                                                                                                 CAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCAC
                                                                                                                                                              MetGluArgProAlaAsnCysMetAspLeuPheAspMetValSerValHisGlyProLeu
                                                                                                                                                                               CTGGAGAGGCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACGGAAAGGGGGAGCCCTG
                                                                                                                                                                                                                   IleProGlyValIleLysIleLeuAspTrpPheAlaAsnSerLysGlyPheLeuIleVal
                                                                                                                                                                                                                                                                                                             CTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGT
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                                                                          AAC---TGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAAT
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US-10-705-757-1 (1-2623) x T13741 (1-1398) Oy 27 AGCGGCGGCGGGCGGACCGGCAGCAGCAGCAGCAGCAGCA	RESULT 7 T13741 hypothetical protein 22E5.8 - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 C;Accession: T13741 R;Murphy, L.; Harris, D.; Barrell, B. submitted to the EMBL Data Library, April 1999 A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: Z17668 A;Accession: T13741 A;Reference number: Z17668 A;Accession: T13741 A;Residues: 1-1398 <mur> A;Residues: preliminary; translated from GB/EMBL/DDBJ A;Cross-references: UNIPROT:077268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA2 C;Genetics: A;Cross-references: UNIPROT:077268; EMBL:AL031765; NID:e1371523; PID:e1329905; PIDN:CAA2 C;Genetics: A;Cross-references: PlyBase:FBgn0000667 A;Introns: 205/3; 227/1; 322/3; 688/3; 782/3; 814/2; 1363/3 A;Note: EG:22E5.8 Alignment Scores: Pred. No.: 402.00 Matches: Pred. No.: 402.00 Matches: 123 Bercent Similarity: 43.82% Gomery Match: 8.39% Gomery Match: 96 Gaps: 17</mur>	Db 175 ThrGlyGluValLysLeuValAspPheGlyAlaThrAlaGluLysAlaThrLys 194 945 ACGGACTTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTAC 1004 195 LysGluPheGlnGlyThrArgSerTyrCysProProGluTrpPheArgAspGInLeuTyr 214 Qy 1005 CATGGCAGGTCGGCGGAGTCTGGTCCCTGGGATCCTGTATGATATGTTGTGGA 1064 215 LeuProLeuGluAlaThrSerTrpSerLeuGlyValLeuLeuPheIleLeuLeuThrGly 234 Qy 1065 GATATTCCTTTCGAGCATGAGAAGATCTCATGAGGGCCAGGTTTTCTTCAGGCAGAGG 1124 1126 GATATTCCTTTCGAGCATGACGAAGAATCCATCAGTGGCCTGGCTTTCTTCAGGCAGAGG 1124 Qy 1065 GATATTCCTTTCGAGCATGACGAAGAATCCTAGTATGAATGGTTGTTGGCCCTGAGACCATCAGAGG 1124 235 LysLeuProPheArgAsGGUIleGInIleCysLeuGlyAsnValLysPheProProAsp 254 Qy 1125 GTCTCTTCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGG 1184 255 LeuSerLysGluValCysGlnLeuValLysSerCysLeuThrThrSerThrSerAlaArg 274 Qy 1185 CCAACCTTCGAGAAAATCCAGGAACCATCCATGGATGCAA 1223 275 AlaSerLeuAlaGlnIleAlaAlaHisProTrpMetGlu 287
		Db 105

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protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_ch
C;Accession: 149072
R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed
A;Reference number: 149071; MUID:95200798; PMID:7893599
A;Accession: 149072
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A, Molecule type: mRNA
A, Residues: 1-481 < RESS-
A;Cross-references: EMBL:U11494; NID:g595420; PIDN:AAA67926.1; PID:g595421
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN>
F;79-87/Region: protein kinase ATP-binding motif
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LeuAlaAlaGluArgAlaValAlaSerArgVal----
    GAGGCCGTGCGGCACTGCCACAACTGCGGGGTGCTACACCGCGACATCAAGGACGAAAAAC
                                                                                  LysAspMetLeuTyrIleValThrGluPheAlaLysAsn---GlyGluMetPheAspTyr
                                                                                                                                                                     CTGAAGAAGGTGAGCTCGGGTTTCTCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGG
                                                                                                                                                                                                                         CGGATTTCCGACTGGGGAGAGCTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTG
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                              LeuThrSerAsnGlyHisLeuSerGluAsnGluAlaArgGlnLysPheTrpGlnIleLeu
                                                        ATCACGGAAAGGGGAGCCCTGCAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTG
                                                                                                              CCCGACAGTTTCGTCCTGATCCTGGAGAGGGCCCGAGCCGGTGCAAGATCTCTTCGACTTC
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26.89%
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R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halfc
Gene 120, 249-254, 1992
A;Title: Structure and expression of a gene
A;Reference number: JC1446; MUID:93013041; P
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEG>
                                                                                            serine/threonine-specific protein kinase (EC 2.7.1. N;Alternate names: protein kinase SNF1 homology C;Species: Arabidopsis thallans (mouse-ear cress) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 C;Accession: JC1446; S58266; S66334
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1206 AACCATCCATGGATGCAA-----GATGTTCTCCTGCCCCAGGAAACTGCTGAGATCCAC
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---CysProGlnProGlnAlaLeuAlaGlnSerValLeuGlnAlaGluIle
                                                      AGGTGTCCA-----
                                                                                                            IleLeuProCysAspProPheArgProSerLeuLeu
                                                                                                                                              TGACTCTCCAGGGGTCCT---AGGCCTCCAACTCCTCCCATAGATACTCTCTTCTTCAT
                                                                                                                                                                                                                     AspLeuSerSerLeuGluValPro-
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|LeuIleArgArgMetLeuValValAspProAlaLysArgIleThrIleAlaGlnIleArg
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M.; Halford, N.G.; Kreis,

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A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g16660d R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P. submitted to the EMBL Data Library, May 1995

A;Description: Differential accumulation of the transcripts of 22 novel protein kinase g A;Pescesion: $58266

A;Accession: $58266

A;Accession: $58266

A;Accession: $58266

A;Accession: $144-198 GTHU>
A;Accidues: 144-198 GTHU>
A;Accidues: 144-198 GTHU>
A;Accidues: 144-198 GTHU>
A;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, $51-565, 1995

A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes in A;Accession: $56334

A;Accession: $56334

A;Accession: $56334

A;Accession: $56334

A;Accession: $56334

A;Accession: $56334

A;Accession: $6471; 125/3; 186966; NID:g928909; PIDN:CAA60529.1; PID:g928910

C;Comment: This enzyme plays an important role in a signal transduction cascade regulating Gene: AKin10; AKZ1

A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3

C;Function:
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology of KINS
P;25,13/Recion: nrotein kinase homology of KINS
Finding motif
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                                                CCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGCGAGCTCAAGCTCAT
                                                                                                               CAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACCACCACTGCCGGGGTGCTACA
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            probable serine/threonine-specific protein kinase N;Alternate names: SNF1-related protein kinase C;Species: Chromis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T10449 R;Gumpel, N.J.
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cucumber

09-Jul-2004

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A;Reference number: Z17020
A;Accession: T10449
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Gross-references: UNIPROT:P93113; EMBL:Y10036
A;Cross-references: UNIPROT:P93113; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
A;Experimental source: cv. Masterpiece; protein kinase homology
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATF; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
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                                                                             GGCCAGGTTTTC---TTCAGGCAGAGGGTCTCTTCAGAATGTCAGCATCTCATTAGATGG
                                                                                                          CysGlyThrLeuProPheAsp---AspGluAsnIleProAsnLeuPheLysLysIleLys
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hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Uul-1996 #sequence_revision 12-Uul-1996 #text_change 16
C;Accession: S66730
R;Ansorge, W; Benes, V; Rechmann, S.; Schwager, C.; Teodoru, C.;
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS>
A;Cross-references: UNIPROT: (O8217; EMBL: Z74788; NID: g1419846; PID:
A;Cross-references: SGD: S0005405

A;Cross-references: SGD: S0005405
                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 15L
C;Superfamily: protein kinase homology
C;Keywords: ATP
P;839-1099/Domain: protein kinase homology <PF;847-855/Region: protein kinase ATP-binding
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Best Local Similarity:
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submitted to the EMBL Data Library, Oc A;Reference number: Z18997
A;Accession: T18611
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Experimental source: clone AH10
A;Experimental source: clone GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: D
                                                                                                                                                                                                                                                                                                                                                           probable serine/threonine-specific protein kinase (EC 2.7.1.-), N;Contains: probable serine/threonine kinase, short splice form C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #eequence revision 15-Oct-1999 #ext_change C;Accession: T18611; T18610; T23144; T23143

R;McMurray, A.
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                                                      PIDN:CAB54178.1;
                                                                                                                                                                                                    EMBL: 281027;
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                                                      GSPDB:GN00023; CESP:H39E23.1b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Experimental source: clone C;Genetics:
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A;Molecule type: DNA
A;Residues: 1-487,536-1192 <WIL4>
A;Cross-references: EMBL:Z96102; PIDN:
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A;Cross-references: EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023;
A;Experimental source: clone H39E23
A;Accession: T23143
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A;Accession: T23144
A;Status: translated from GB/EMBL/DE
A;Molecule type: DNA
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probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potato
N;Alternate names: StubSNF1 protein
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07788
R;Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A;Reference number: Z16133
A;Accession: T07788
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <LAK>
A;Gene: SNF1
C;Genetics:
C;Genetics:
C;Genetics:
A;Gene: SNF1
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
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probable serine/threonine protein Kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YALO02; protein YALO17w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1993 #sequence revision 02-Aug-1994 #text_change 16-Aug-2004
C;Accession: S33553; S36717; S36732; JH0408
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac yeast 9, 543-549, 193
A;Tille: The YALO17 gene on the left arm of chromosome I of Saccharomyces cerevisiae enc A; Reference number: S3353; MUID:93311122; PMID:8322517
A;Accession: S3353; MUID:93311122; PMID:8322517
A;Accession: S3353; MUID:93311122; PMID:8322517
A;Accession: S3353; MUID:93311122; PMID:8322517
A;Accession: S36732; MUID:9331112; PMID:8322517
A;Accession: Sequence not shown
A;Clark, M.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; D
Submitted to the EMBL Data Library, January 1993
A;Beference number: S36711
A;Accession: S940511
A;Accession: S940571358 cOUE>
A;Reference number: S36711
A;Accession: S3672
A;Title: Identification of a Saccharomyces cerevisiae homolog of the SNF2 transcriptiona
A;Reference number: S22266; MUID:92221690; PMID:1561836
A;Recession: S3673
A;Residues: 1-162 c(715)
A; Cross references: EMBL:S93805

R, Sidhu, R.S.; Mathewes, S.; Bollon, A.P.

Gene 107, 111-118, 1991

A; Title: Selection of secretory protein-encoding genes by fusion with PHO5

A; Meference number: JH0483; MUID:92077420; PMID:1743509

A; Recession: JH0486

A; Molecule type: DNA

A; Residues: 1-72, 'E', 74-154 <SID>
C; Genetics:
A; Gene: SGD:FUN31; SSP138

A; Cross-references: SGD:S0000015; MIPS:YAL017w

A; Map position: IL
C; Superfamily: protein kinase homology
C; Keywords: ATP; glycoprotein; phosphotransferase; serine/threonine-specification: IR
C; Superfamily: protein kinase homology
C; Keywords: ATP; glycoprotein kinase homology <KIN>
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Residues: 1-862 <CL2>
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ArgCysValProLysArgProThrIleAspAspIleAsnAsnAspLysTrpLeu
                             PheAsnAsnAlaGluGluValSerGluAspCysIleGluLeuIleLysSerIleLeuAsn
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serine/threonine-specific protein kinase (EC 2.7.1. N;Alternate names: SNF1 protein kinase omolog AKINI C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 C;Accession: T52633

2.7.1.-)
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R;Bhalerso, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machid Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999
A;Title: Regulatory interaction of PRLI WD protein with Arabidopsis SNF1-like protein ki A;Accession: T52633
A;Accession: T52633
A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-512 <a href="https://doi.org/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/10.1002/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-705-757-1 (1-2623) x T52633
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                                                      IleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAsp---AspGluAsnIleProAsn
                                                                                                                                                                GluvalileSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSerCysGlyVal
                                                                                                                                                                                                                    GAGTGGATCCGCTACCATCGCTACCATGGCAGGTCGGCGGCAGTCTGGTCCCTGGGGATC
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                                                                                                          CTGCTGTATGATATGGTGTGGAGATATTCCTTTCGAGCATGACGAAGAGATC-----
                                                                                                                                                                                                                                                                                                                                                                                     AsnLeuLeuLeuAsp---SerArgCysAsnIleLysIleAlaAspPheGlyLeuSerAsn
-----ATCAGGGCCAGGTTTTC---TTCAGGCAGAGGGTCTCTTCAGAATGT 1139
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416 uLeuAsnValCysTrpLysLys
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Search completed: September 22, 2005, 17:20:15
Job time: 115.96 secs

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Commtand line parameters:

-MOLEL=frame+ n2p.model -DEV=xlp
-MOLEL=frame+ n2p.model -LOOPEXT=0
-CGN2_1/USF02_0 =Bool_p/US10705757/runat_22092005_115015_22129/app_query.fasta_1.5333
-De-Unify=2010 -SFART=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pot -NORM=ext -HEAPSIZE=500 -MILLEN=0 -MAXLEN=2000000000
-USER=US10705757 @CGN 1 1 980 @runat 2209205_115015_22129 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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PIM3_COTUA
PIM3_HUMAN
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PIM3_RAT
QB11X8
PIM2_MOUSE
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felis silve
bos taurus
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drose	Q96rg2 homo sapien	Q9v8v8 drosophila	-	Q6npa6 drosophila	Q76n03 homo sapien	Q8cic0 mus musculu	Q7krk3 drosophila	_			Q641k5 mus musculu	dros		yarr		dros		cani	Q6p2j9 homo sapien	mue i	-	Q8t3f1 caenorhabdi	Q20443 caenorhabdi		Q6di52 brachydanio		Q8jfw9 brachydanio	Q7zvj5 brachydanio

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ID PINI HUMAN STANDARD; PRT; 313 AA.
AC P113\overline{O}9; Q96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 13, Last sequence update)
DT 01-JUL-2004 (Rel. 44, Last annotation update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
[4]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88115604; PubMed=3429489;
Meeker T.C., Nagarajan L., Ar-Rushdi A., Croce C.M.;
Meeker T.C., Nagarajan L., ar-Rushdi A., Croce C.M.;
"Cloning and characterization of the human PIM-1 genumber of the protein kinases.";
                                                                                                                                                                                                                                                                                                                                                                  Domen J., von Lindern M., RELINGUIS A., PORTON A.;

Berns A.;

"Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence in the invitro synthesized PIM-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=87277423; PubMed=3475233; DOI=10.1016/0378-1119(87)90352-0; Zakut-Houri R., Hazum S., Givol D., Telerman A.; Takut Bequence and gene analysis of the human pim oncogene."; Gene 54:105-111(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE=90382681; PubMed=2205533; DOI=10.1016/0378-1119(90)90195-W;
Reeves R., Spies G.A., Kiefer M., Barr P.J., Power M.;
"Primary structure of the putative human oncogene, pim-1.";
Gene 90:303-307(1990).
[2]
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                          and immunological identification protein.";
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                                                                                                                                                                                                                                                                                                                Oncogene Res. 1:103-112(1987).
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Primates;
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RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schemtz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schemtz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-202 FROM N.A.

MEDLINE=21354098; PubMed=11460166; DOI=10.1038/35085588;
Pasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
"Hypermutation of multiple proto-oncogenes in B-cell diff_cell lymphomas.";
Nature 412:341-346(2001).
                                                                             Telerman A., Amson R., Zakut-Houri R., Givol D.; "Identification of the human pim-1 gene product as a cytoplasmic protein with tyrosine kinase activity."; Mol. Cell. Biol. 8:1498-1503(1988).
                                                                                                                                                                                                                                                                                                                                                                  phosphorylation
phosphorylation
HP1(1).";
                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20130009; PubMed=10664448; DOI=10.1016/S0014-5793(00)01105-4; Koike N., Maita H., Taira T., Ariga H., Iguchi-Ariga S.M.M.; "Identification of heterochromatin protein 1 (HPI) as a phosphorylation target by Pim-1 kinase and the effect of phosphorylation on the transcriptional repression function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION.
MEDLINE=88246418; PubMed=2837645;
                                                                                                                                                                                                                                                          MEDLINE=22567470; PubMed=12680209;
IONOV Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder Johnson T., Lilly M.B., Kraft A.S.;
"Pim-1 protein kinase is nuclear in Burkitt's lymphoma: nuclear
            This SWISS-PROT entry
                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                      FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                      DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.; WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIMIID261.html".
the Swiss Institute of Bioinformatics
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EMBL; M16750; AAA60089.1; -.
EMBL; M54915; AAA36447.1; -.
EMBL; M24779; AAA81553.1; -.
EMBL; BC020224; AAH20224.1; -.
EMBL; AF386792; AAK70871.1; -.
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PROSITE; PS50011; PROTI
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GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PS50011; PROTEIN KINASE DOM; 1
PS00108; PROTEIN KINASE ST; 1.
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                                   TCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTG
                                                                                                   ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe
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ATP (By similarity).
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EMBL; AB073740; BAB71752.1; -.

EMBL; AB073740; BAB71752.1; -.

InterPro; IPR011009; Kinase_like.
                                                                                                                                                                                                                                      Q951.70;
28-PEB-2003 (Rel. 41, Created)
28-PEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pelis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Pissipedia; Felidae;
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InterPro; IPR008271; Ser thr_pkin_AS.

Pfam; PF00069; Pkinase; I.

ProDom; PD000001; Prot kinase; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS00107; PROTEIN KINASE DOM; I.

PROSITE; PS00108; PROTEIN KINASE ST; I.

PROSITE; PS00108; PROTEIN KINASE DOM; I.

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ATP (By similarity).
Proton acceptor (By similarity);
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HSSP; 063450; 1A06.

InterPro; IPR011009; Kinase_like.

InterPro; IPR0010719; Prot Kinase.

InterPro; IPR000719; Prot Kinase.

InterPro; IPR008271; Ser Chr_pkin_AS.

Pfam; PF00069; Pkinase; I.

ProDom; PD000001; Prot Kinase; I.

ProDom; PD000001; Prot Kinase; I.

PROSITE; PS00107; PROTEIN_KINASE_DOM; I.

PROSITE; PS00108; PROTEIN_KINASE_ST; I.

PROSITE; PS00108; PROTEIN; Phosphorylation; Prospine Serine/threonine-protein kinase; Transferase.

DOMAIN

BIND

44

52

ATP (By similarity).

BINDING

67

ATP (By similarity).
                                                                                     NP BIND
BINDING
ACT SITE
SEQUENCE
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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28-FEB-2003
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Mammalia; Eutheria;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-Sprague-Dawley; TISSUE-Testis;

STRAIN-Sprague-Dawley; TISSUE-Testis;

Wingett D., Reeves R., Magnuson N.S.;

Wingett D., Reeves R., Magnuson N.S.;

Characterization of the testes specific pim-1 transc

Nucleic Acids Res. 20:3183-3189(1992).

Nucleic Acids Res. 20:3183-3189(1992).

-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a pho-

-I- SUBUNIT: Binds to RP9 (By similarity).

-I- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (B)

-I- PTM: Autophosphorylated (By similarity).

-I- SIMILARITY: Belongs to the Ser/Thr protein kinasc

-I- SIMILARITY: Belongs to the Ser/Thr protein kinasc
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ProDom; PD000001; Proct kinase; I.

PROSITE; PS00107; PROTEIN KINASE ATP; I.

PROSITE; PS00101; PROTEIN KINASE DOM; I.

PROSITE; PS00108; PROTEIN KINASE ST; I.

PROSITE; PS00108; PROTEIN KINASE; Transferase.

BY BIND 34 290 Protein kinase; Interest Strates Strate
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Name=Pim1, Synonyms=Pim-1;
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Rodentia; S
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X63675; CA
PIR; S26298; S26
RGD; 3330; Pim1.
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BINDING
ACT_SITE
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01-AUG-1992 (Rel.
05-JUL-2004 (Rel.
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IPRO11009; Kinase Line.
IPRO00719; Prot Kinase.
IPR008271; Ser thr pkin AS
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serine/threonine-protein kinase
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IP (By similarity).
roton acceptor (By similarity)
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Matches:
Conservative:
Mismatches:
Indels:
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STRAIN=C57BL/6; TISSUE=Brain, and Eye;

STRAIN=C57BL/6; TISSUE=Brain, and Eye;

STRAIN=C57BL/6; TISSUE=Brain, and Eye;

STRAIN=C57BL/6; TISSUE=Brain, and Eye;

MEDLLINE=233B8257, PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.L., Sheamen C.M., Schuler Klausener R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F
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C.F., Bhat N.K.,
J., Hsieh F.,
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ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKc; 1.

SMO210; STKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-prot SEQUENCE 313 AA; 35451 MW; 1294F16A03F
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MGD; MG1:97584; PHM1
GO; GO:0005524; F:ATP
GO; GO:0004674; F:Tran
GO; GO:0016740; F:Tran
GO; GO:0006469; F:Drot
GO; GO:0006469; F:Drot
GO; GO:0006469; F:Tran
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ d
-!- SIMILARITY: Belongs to the Ser/Thr protein
EMBL; BC042885; AA442885.1; -.
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"Generation and initial analysis
and mouse CDNA sequences.";
proc. Natl. Acad. Sci. U.S.A. 99;
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STRAIN=C57BL/6; TI
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Submitted (JAN-2003)
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GO:0005524; P:ATP binding; IEA.
GO:0004574; F:protein serine/threonine kinase acti
GO:0016740; F:transferase activity; IEA.
GO:0006468; P:protein amino acid phosphorylation;
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L; BC055316;
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                                                                     ATGCTCTTGTCCAAAATCAACTCGCTTGCCCACCTGCGCGCCCCGCCCCTGCAACGACCTG
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IPR0082290; Ser thr pkinase.
IPR008271; Ser thr pkin_AS.
0069; Pkinase; I.
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; AAH42885.1; -.
; AAH53019.1; -.
; AAH55316.1; -.
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SEQUENCE FROM N.A.
MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.
Selten J., van Beveren C., Berns A.;
The primary structure of the putative oncogene pim-1 shows extensi
                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                     Name=Pim1; Synonyms=Pim-1;
Mus musculus (Mouse).
                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
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InterPro; IPRO00719; Prot kinase.
InterPro; IPRO00719; Prot kinase; I.
ProDom; PD000009; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
PROSITE; PS00101; PROTEIN KINASE TOM; I.
PROSITE; PS0011; PROTEIN KINASE ST; I.
PROSITE; PS00108; PROTEIN KINASE ST; I.
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Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
"PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
Eur. J. Biochem. 267:5168-5178(2000).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Binds to RP9.
-!- SUBUNIT: Binds to RP9.
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- PTM: Autophosphorylated (By similarity).
-!- DISEASE: Frequently activated by provirus insertion in murine leukemia virus-induced T-cell lymphomas.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M13945; AAA39930.1;
PIR; A24169; TVMSP1.
HSSP; Q63450; 1A06.
MGD; MGI:97584; Pim1.
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RESULT 7
PIM3_COTJA
MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355; Bichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.; "Developmental expression of Pim kinases suggests functions al outside of the hematopoietic system."; Oncogene 19:1215-1224(2000).
-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote:
-i- PTM: Autophosphorylated.
                                                                                                                                                                                                                                                                                                                                                                              PIM3_COTUA
Q9PU85;
                                                                                                                                                                                                                     Name=PIM3; Synonyms=PIM-3;
Coturnix coturnix japonica (Japanese quail).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Serine/threonine-protein kinase Pim-3
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INTERTPRO; IPRO11009; Kinase like.
INTERTPO; IPRO10719; Prott_Kinase.

INTERTPO; IPR000219; Ser_thr_pkinase.

INTERTPO; IPR002290; Ser_thr_pkin_AS.

R Pfam; PF000069; Pkinase; 1.

R ProDom; PD000001; Prott_kinase; 1.

R PROSITE; SM00220; S_TKC; 1.

JR SMART; SM00220; S_TKC; 1.

JR PROSITE; PS001107; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS001108; PROTEIN_KINASE_ST; 1.
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IFP (By similarity).
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Conservative:
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RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899; RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., RA Stauener R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., RA Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J., RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Tolkson B.J., Lu X., Gibbs R.A., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., R. Scherch J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., Shelin J.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Shelin J.E., Schnerch J.E., Jones S.J.M., Marra M.A., Shelin J.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Shelin J.E., Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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086V86;
29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
IDENTIFICATION FROM ESTS.

MEDILINE=22682943; PubMed=12798037; DOI=
Chichester C., Nikitin F., Ravarini J.-
"Consistency checks for characterizing
Comput. Biol. Chem. 27:29-35(2003).
-!- CATALYTIC ACTIVITY: ATP + a protein
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                  DOI=10.1016/S1476-9271
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zing protein forms.";
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Phosphorylation; Serine/threonine-protein
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InterPro; IPR0011009; Kinase like.
InterPro; IPR00719; Prot kinase.
InterPro; IPR008271; Ser thr pkin_AS.
Pfam; PP00069; Pkinase; I.
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ATP (By similarity).
Proton acceptor (By similarity).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PIM3 MM SETTING MUSE ID PIM3 M AC P58750
DT 28-FEB DT 28
                                                                                                                                              RC STRAIR=FVBN, TISSUE=Colon, and Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Magner L., Sheneen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheneen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulhy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulhy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulhy S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Witting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Holterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
   This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
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STRAIN=FVB/N; TISSUE=Colon,
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Mammalia; Eutheria;
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Best Local Similarity:
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Pred. No.:
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HSSP; 003656; 1HOW.
InterPro; IPR011009; Kinase_like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR000271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
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SMART; SM00220; S_TKC; 1.

PROSITE; PS0010; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Phosphorylation; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                    CGGCACTGCCACACTGCGGGGTGCTACACCGCGACATCAAGGACGAAAACATCCTTATC
                                                                                                                 PheLeuLeuValLeuGluArgProGluProAlaGlnAspLeuPheAspPheIleThrGlu
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
DD68CBF46354851E CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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EMBL; AF086624; AAC68900.1; A
EMBL; AF057026; AAC36065.1; HSSP; Q03656; 1HOW.
RGD; 620462; Pim3.
InterPro; IFR011009; Kinase 1
InterPro; IFR000719; Prot kIn
InterPro; IFR008271; Ser_thr_

Kinase like. Prot_kinase. Ser_thr_pkin_AS.

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070444;

070444;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

05-JUL-2004 (Rel. 44, Last annotation update)

Serine/threonine-protein kinase Pim-3 (BC 2.7.1.:

Kid-1) (Kinase induced by depolarization).

Name=Pim3; Synonyms-Kid1;

Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND CHARACTERIZATION.

MEDLINE-98298176; PubMed=9632723; DOI=10.1074/jbc.273.26.16535;
Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L
Bazan N.G., Baudry M., Herschman H.R.;
Bazan N.G., Baudry M., Herschman H.R.;
"KID-1, a protein kinase induced by depolarization in brain.";
"KID-1, a protein kinase induced by depolarization in brain.";
J. Biol. Chem. 273:16535-16543 (1998).

-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein
-!- TISSUS SPECIFICITY: Present in a number of unstimulated tissues.
                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Sprague-Dawley;
Konietzko U., Kuhl D.;
"Pim-3 is a member of
Submitted (AUG-1998) t
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: By membrane depolarization PTM: Autophosphorylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          including brain.
INDUCTION: By men
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BINDING
ACT SITE
SEQUENCE
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Pfam; PF00069; pkinase; 1.

ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN KINASE_ST; 1.

ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
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ATP (By similarity).
Proton acceptor (By similarity).
DD6C9BP4635P851E CRC64;
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C. -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family RMBL; AV026239; AAK16606.1; -.

R HSSP; 003656; 10999

R MGD; MGI:1355297; Pim3.

R GO; GO:0004674; F:ATP binding; IEA.

R GO; GO:00046740; F:transferase activity; IEA.

R GO; GO:00046740; P:transferase activity; IEA.

R GO; GO:0006740; P:transferase activity; IEA.

R GO; GO:0006780; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006781; P:protein amino acid phosphorylation; IEA.

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006471; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006471; P:protein amino acid phosphorylation; IEA.

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006471; P:protein amino acid phosphorylation; IEA.

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0016740; P:transferase activity;

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0016740; P:transferase activity;

R GO; GO:0016740; P:transferase activity;

R GO; GO:000648; P:protein amino acid phosphorylation; IEA.

R GO; GO:0016740; P:transferase activity;

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Q811X8;
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01-JUN-2003
01-MAR-2004
KID1.
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Mammalia; Eutheria;
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a collaboration BL outstation -ictions on its

kinase;

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DT 15-DEC
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37)
                                                            Pim-1 proto-oncogene-encoded protein kinase.", J. Biol. Chem. 272:105.14-10521(1997).
-I- CATALYTIC ACTIVITY: ATP + a protein = ADP - I- PTM: Autophosphorylated.
-I- SIMILARITY: Belongs to the Ser/Thr protein
                                                                                                                                                                                 SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalnar G., Tai G., Oh S., Amankawa L., Affolter M.
Aebersold R., Pelech S.L.;
                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                               Name=PIM3; Synonyms=PIM1; Xenopus laevis (African clawed frog).
                                                                                                                                                               "Identification of the autophosphorylation
                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
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subfamily.

CAUTION: Was originally (Ref represent the pim-3 isoform.
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BINDING
ACT_SITE
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Probom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Phosphorylation; Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser thr pkin
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                                                                                                                                                                                                                                                                                                                                                                                                                             MetLeuLeuSerLysPheGlySerLeuAlaHisIle-----CysAsnProSer
                          GluLysGlyProLeuAspGluAspThrAlaArgGlyPhePheArgGlnValLeuGluAla
                                                                GANAGGGGAGCCCTGCAAGAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCC
                                                                                                       TCCGACTGGGGAGAGCTGCCTAATGGCACTCGAGTGCCCATGGAAGTGGTCCTGCTGAAG
                                                                                                                                                                                                                                                                                                                                               AspSerArgIleAlaAspGlyGlnProValAlaValLysHisValAlaLysGluArgVal
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Phosphoserine (by autocatalysis).
Phosphothreonine (by autocatalysis)
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
Phosphoserine (by autocatalysis)
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                                                                                                                                                                    RC TISUE-Embryo;
RC TISUE-Embryo;
RX PubMed=12477992; DOL=10.1073/pnas.242603899;
RX PubMed=12477992; DOL=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Strausberg R.L., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RX Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hosg L.,
RX Alteschul S.F., Jordan R., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RX Stapleton M., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RX Raha J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RX Pahey J., Halten S., Garben B.D., Dickson M.C.,
RX Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RX RAM, Kraywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E.,
RX Arnes S.J. Warra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q66III, PRELIMINARY; PRT; 318 AA.
Q66III, 261III, 27.0CT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
    SEQUENCE FROM N.A.
TISSUE=Embryo;
Klein S., Gerhard D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
NCBI_TaxID=8364;
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                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000
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                                                                                                               cDNA sequences.";
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InterPro; IPR001009; Kinase like.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase; 1.
Pr000m; P000001; Prot_kinase; 1.
ProDom; P0000001; Prot_kinase; 1.
SMART; SM00219; Tyr6; 1.
SMART; SM00219; Tyr6; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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ATCCTGCTGTATGATATGGTGTGTGGAGATATTCCTTTCGAGCATGACGAAGAGATCATC
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EMBL; L41495; AAA98923.1; -.

EMBL; L41495; AAA98924.1; -.

PIR; S5333; S5333.

HSSP; Q63450; 1A06.

MGD; MGI:97587; Pim2.

G0; G0:0005515; P:protein binding; IPI.

G0; G0:0004674; P:protein serine/threonine kinase acti

G0; G0:0006916; P:anti-approcis; IDA.

G0; G0:0008671; P:appotetic mitochondrial changes; IDA

InterPro; IPR011009; Kinase like.

InterPro; IPR008271; Ser_thr_pkinas.

InterPro; IPR008219; Ser_thr_pkinase.

PEDD00069; Pkinase; I.

InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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EMBO J. 1
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MEDLINE-95300786; PubMed=7781606;

van der Lugt N.M., Domen J., Verhoeven E., Linders K.,

van der Gulden H., Allen J., Berns A.;

"Proviral tagging in E mu-myc transgenic mice lacking "proviral tagging in E mu-myc activation of Pim-2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIM2 MOUSE STANDARD; PRT; 370 AA. 062070; Q62071; Q62072; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) serine/threonine-protein kinase Pim-2 (EC 2.7.1.37).
ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; S TKG; 1.

PROSITE; PS001017; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

Alternative initiation; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse).
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CATALYTIC ACTIVITY: ATP + a
ALTERNATIVE PRODUCTS:
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Comment=3 isoforms, 1 (show
alternative initiation. Iso
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RC STRAIN=FVB/N; TISSUB=Mammary tumor. C3;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkine R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkine R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casvant T.L., Scheetz T.E.,

RA Richards S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.R., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.R., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Pahey J., Helton E., Ketteman M., Madan A., Gorigues S., Sanchez A.,

RA Rating M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Pan Rating M., Schalka U., Smailus D.E., Schnerch A., Schein J.E.,
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01-JUN-2002
01-JUN-2002
01-OCT-2003
Strausberg R.;
Submitted (APR-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (Mouse)
                              SEQUENCE FROM N.A.
STRAIN-FVB/N; TISSUE-Mammary
                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis
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R InterPro; IPR001719; Prot kinase.

InterPro; IPR0002790; Ser thr pkinase.

InterPro; IPR000271; Ser thr pkinase.

InterPro; IPR008271; Ser thr pkinase.
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ProDom; PD000001; Prot kinase; 1.

SMART; SM00220; STKc; I.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 311 AA; 34486 MW; P7B770908D23A710 CRC64;
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Search completed: September 22, 2005, 17:14:39 Job time : 452.035 secs

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Command line parameters:

-MODEL-frame+ nip.model pUSU-705757/runat 22092005 115016 22174/app query.fasta_1.5333
-Q-/cgn2 1/USPTO_spool p/USU-705757/runat 22092005 115016 22174/app query.fasta_1.5333
-DB-Published_Applications_AA -OFMT-fastam -SUFFIX=nip.rapb -MINMATCH=0.1
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-45 -DOCALIGN=200 -THR SCORE-pct -THR MXX=100
-THR MIN=0 -ALICH=15 -MODE-LOCAL -OUTFMT-pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER-US10705757 @CGN 1 1 743 @runat 22092005 115016 22174
-NCPU-6 -ICPU-3 -NO_MAAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XAAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2005 Compugen Ltd.
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10R_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10R_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

US-09-971-791-9

Sequence 9, Application US/09971791 Patent No. US20020115120A1

```
GENERAL INFORMATION:

APPLICANT: LAURA A. Rudolph-Owen

APPLICANT: Kyle.MacBeth
APPLICANT: Kyle.MacBeth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEILE REFERENCE: 35800/23885

FULE REFERENCE: 35800/23885

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT FILING DATE: 2001-10-04

PRIOR APPLICATION NUMBER: 09/644,450

PRIOR FILING DATE: 2000-08-23

PRIOR FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 313
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; TYPE: PRT
; ORGANISM: Homo
US-09-971-791-9
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Best Local Similarity:
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TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGC
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; Publication No. US20030045491A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
; TITLE OF INVENTION: TTK in Diagnosis and as
; TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
; CURRENT APPLICATION NUMBER: US/10/081,119
; CURRENT FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR PILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR PILING DATE: 301-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR PILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR PILING DATE: 2001-02-21
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR PILING DATE: 2001-02-21
; CURRENT FILING DATE: 2001-02-21
; CURRENT FILING DATE: 2001-02-21
; PRIOR PILING DATE: 2001-02-21
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Sequence 52, Application US/10394322A
Publication No. US20030232391A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: PRESCOCK, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INF
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 313
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ORGANISM: Homo
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Sequence 13, Application US/10348081
Publication No. US20040038246A1
GENERAL INFORMATION:
APPLICANT: KORN, MARCUS
APPLICANT: KORN, MARCUS
APPLICANT: SCHNEIDER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                          RESULT 4
US-10-348-081-13
                                             SEQ ID NO 13
LENGTH: 313
TYPE: PRT
ORGANISM: Homo :
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US-10-664-421-1

| Sequence 1, Application US/10664421
| Sequence 1, Application US/10664421
| Publication No. US20040142864A1
| GENERAL INFORMATION:
| APPLICANT: BERMER, RYAN
| APPLICANT: KUMAR, ABHINAV
| APPLICANT: MANDIYAN, VALSAN
| APPLICANT: MILBURN, MICHAEL V.
| TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM
| FILE REFERENCE: 039363/0703
| CURRENT APPLICATION NUMBER: US/10/664,421
| CURRENT APPLICATION NUMBER: 60/412,341
| PRIOR APPLICATION NUMBER: 60/412,341
| PRIOR APPLICATION NUMBER: 60/412,341
| PRIOR FILING DATE: 2002-09-16
| PRIOR APPLICATION NUMBER: 60/412,341
| PRIOR FILING DATE: 2002-09-16
| NUMBER OF SEQ ID NOS: 169
| SOFTWARE: PatentIn Ver: 3.2
| SEQ ID NO 1
| LENGTH: 313
| TYPE: PRT
| ORGANISM: Homo Sapiens
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GAGCTCAAGCTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACCGTCTACACGGAC

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APPLICANT: IBRMER, RYAN
APPLICANT: KUMAR, ABHINAY
APPLICANT: KUMAR, ABHINAY
APPLICANT: KUMAR, ABHINAY
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PATENTING DATE: 2002-09-16
ORGANISM: Homo Bapiens
US-10-664-421-150
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Sequence 9, Application US/10377268
Publication No. US20040171062A1
GENERAL INFORMATION:
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: MILBURN, MICHAEL VANCE
ITITLE OF INVENTION: METHOD FOR THE DESIGN OF
FILE REFERENCE: 039363/0303
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR FILING DATE: 2003-01-02
PRIOR FILING DATE: 2003-01-02
PRIOR FILING DATE: 2002-02-28
PRIOR PPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
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                                                                                                                                   TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC
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; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PATENTIN VEY. 2.1
; SEQ ID NO 9
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-377-268-9
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Best Local Similarity:
Query Match:
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Sequence 18, Application US/10951389

Publication No. US20050058627A1

GENERAL INFORMATION:

APPLICANT: Reinhard, Christoph

APPLICANT: Jefferson, Anne B.

APPLICANT: Jefferson, Anne B.

APPLICANT: Chan, Vivien W.

TITLE OF INVENTION: Target in Cancer

FILE REFERENCE: 16932.002

CURRENT APPLICATION NUMBER: US/10/951,389

CURRENT APPLICATION NUMBER: US/10/951,389

CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION UNMBER: US/10/081,389

USMORTHMENT US/1
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Pred. No.:
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; ORGANISM: Homo
US-10-951-389-18
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APPLICANT: Reinhard, Christoph
APPLICANT: Feinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 1992-002
CURRENT APPLICATION NUMBER: US/10/951,406
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 65/20/081,119
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 66/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
TYPE: PAT
ORGANISM: Homo sapiens
US-10-951-406-18
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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RESULT 10
US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
; APPLICANT: Reinhard, Christoph
; APPLICANT: Usfferson, Anne B.
; APPLICANT: Chan, Vivien W.
; TITLE OF INVENTION: TTK in Diagnosis and as
; TITLE OF INVENTION: TTK in Cancer
; FILE REFERENCE: 16912.002
; CURRENT APPLICATION NUMBER: US/10/951,477
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CURRENT FILING DATE: 2004-09-27;
PRIOR APPLICATION NUMBER: US/10/081,119;
PRIOR FILING DATE: 2002-02-21;
PRIOR APPLICATION NUMBER: 60/289,813;
PRIOR FILING DATE: 2001-02-21;
NUMBER OF SEQ ID NOS: 38;
SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 18;
LENGTH: 313
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         CCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT
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; ORGANISM: Homo
US-10-977-087-18
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PRIOR APPLICATION NUMBER: US/10/977,08
PRIOR APPLICATION NUMBER: 10/081,119
PRIOR ELING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/271,254
PRIOR APPLICATION NUMBER: 10/360,848
PRIOR FILING DATE: 2003-02-06
PRIOR PILING DATE: 2003-02-06
PRIOR PILING DATE: 2003-05-06
PRIOR PILING DATE: 2003-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/134,112
PRIOR PILING DATE: 1999-05-14
PRIOR PILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/626,301
PRIOR APPLICATION NUMBER: 09/626,301
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-08-13
PRIOR PILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR FILING DATE: 1999-07-26
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PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-26
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                                                           US-10-705-757-1 (1-2623) x US-10-977-087-18 (1-313)
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SOFTWARE: FAST
SEQ ID NO 18
FRIGHTH: 313
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
TITLE OF INVENTION: AND THEIR METHODS OF USE V
FILE REFERENCE: 2300-21986
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SOFTWARE: FastSEQ for Windows Version 4.0
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No. US20050130926A1
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RESULT 12
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Publication No
APPLICANT: GRI
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PRIOR APPLICA
# Sequence 2, Application US/10705757
# Publication No. US20040146942A1
# GENERAL INFORMATION:
# APPLICANT: GRUENENTHAL GMBH
# TITLE OF INVENTION: SCREENING METHOD USING PI
# FILE REFERENCE: 029310.52818US
# CURRENT APPLICATION NUMBER: US/10/705,757
# CURRENT FILING DATE: 2003-11-12
# PRIOR APPLICATION NUMBER: PCT/EP02/05234
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PRIOR APPLICATION NUMBER: DE 10.
PRIOR APPLICATION NUMBER: DE 10.
PRIOR FILING DATE: 2001-05-11
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: ARTIS, DEAN R.
APPLICANT: BREMER, RYAN E.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: HURT, CLARENCE R.
APPLICANT: HURT, CLARENCE R.
APPLICANT: IBRAHIM, PRABHA L.
APPLICANT: ZUCKERMAN, REBECCA L.
TITLE OF INVENTION: WOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT FILE OF INVENTION NUMBER: US/10/941,635
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2003-09-15
INUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 1
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                        GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp
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GAGAGGCCCGAGCCGGTGCAAGATCTCTTCGACTTCATCACCGGAAAGGGGGAGCCCTGCAA
                                                          TCCGGCGTCATTAGGCTCCTGGACTGGTTCGAGAGGCCCGACAGTTTCGTCCTGATCCTG
                                                                                                                                                                  AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGAGAGCTG
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                                             SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu
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APPLICANT: ARTIS, DEAN R.

APPLICANT: BREMER, RYAN E.

APPLICANT: GILLETTE, SAMUEL J.

APPLICANT: HURT, CLARENCE R.

APPLICANT: IBRAHIM, PRABHA L.

APPLICANT: ZUCKERMAN, REBECCA L.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KIN
FILE REFERENCE: 099363-1702
                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PACENTIN Ver. 3.2
; SEQ ID NO 152
; LENGTH: 313
            Percent Similarity:
Best Local Similarity:
Query Match:
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OTHER INFORMATION:
US-10-941-635-152
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                                                                                           Alignment Scores:
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                                                                                                                                                                                      TYPE: PRT
ORGANISM: Unknown Organism
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Matches:
Conservative:
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RESULT 15
US-10-620-052A-22
i Sequence 22, Application US/10620052A
i Publication No. US20040126784A1
i GENERAL INFORMATION:
i APPLICANT: Hitoshi, Yasumichi
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APPLICANT: Markovtsov, Vadim
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Cellular Pro
FILE REPERENCE: 021044-004010US
CURRENT APPLICATION NUMBER: US/10/620,052A
CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 60/395,443
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 78
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 22
LENGTH: 313
TYPEP: DRT
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mplet : 374	301	1251	281	1191	261	1131	241	1071	221	1011
Search completed: September 22, 2005, 17:46:35 Job time : 374.236 Becs	301 GluileHisLeuHisSerLeuSerProGlyProSerLys 313	1251 GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA 1289	PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300	1191 TTCGAAGAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACCTGCT 1250	261 SerGluCysGlnHisLeuIleArgTrpCysLeuAlaLeuArgProSerAspArgProThr 280	TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC 1190	ProPheGluHisAspGluGluIleIleArgGlyGlnValPhePheArgGlnArgValSer 260	1071 CCTTTCGAGCATGACGAAGAGATCATCAGGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT 1130	221 ArgSerAlaAlaValTrpSerLeuGlyIleLeuLeuTyrAspMetValCysGlyAspIle 240	1011 AGGTCGGCGGCAGTCTGGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGTGGAGATATT 1070

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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USFTO_8pool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-Q=/cgn2_1/USFTO_8pool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-DB=A Geneseq -QFMT-fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=poct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10705757 @CGN 1 1753 @runat 22092005 115014 22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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                                                                                                                                                                                                                  Score
       seq length: 0
seq length: 2000000000
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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Ygapop 10.0,
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Delop 6.0,
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Adf45083 Human Pin
Ad019690 Human PIM
Ad0188370 Human PIM
Adp24227 PRO polyp
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mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
                                                                                                                                                                               WPI; 2002-698650/75.
N-PSDB; ABV73989.
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Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders wi abnormal expression levels and activity of TTK, such as lung, colon,

ovarian

cancer

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Percent Similarity:
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human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method i useful for modulating the level or activity of HKID-1 polypeptide or polynucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the amino acid sequence of a human protein kinase phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disor Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; WM; human.
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23-AUG-2000; 2000US-00644450.
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                                                                                                                                                                                                                                                     The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIMI or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or neurodegenerative diseases). The present sequence is human PIM1 kinase
                                                                                                                                                                                                                                                                                                                                    Method for identifying analgesics, useful particularly for chronic pain, by screening compounds for interaction with E kinase, or related compounds.
                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                          tyrosine threonine kinase; TTK; cancer; cytostatic; checkpoint gene; PIM1.
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Percent Similarity: Best Local Similarity:

7.05e-113 1670.00 100.00% 100.00% 34.87%

Length: Matches: Conservative:

313 0 0 0

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Sequence 313

Query Match:

US-10-705-757-1 (1-2623) x ABU61613

(1-313)

Gaps: Mismatches: Indels:

1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu

20

40 470

60 530 CACGCCACCAAGCTGGCGCCCGGCAAGGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG

. GGCCCGCTACTGGGCAGCGGCGGCTTCGGCTCGGTCTACGCATCCGCGTCTCCGAC

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CC polymuclectide in a test cell obtained from the subject and in a normal connectance cell, where an increase in the expression level of TTK protein cor nucleic acid in the test cell compared to that in the normal cell, cornectates the presence of cancer other than ovarian cancer. Also included care reducing growth of a cancerous cell (by contacting a cancerous cell (comprising: (i) detecting the activity of a cancerous cell (comprising: (i) detecting the activity of a contacting a cancerous cell (comprising: (i) detecting the activity of a contacting a cancerous cell (comprising: (i) detecting the activity of a contacting a cancerous cell (comprising: (i) detecting the activity of a contacting the activity of a contacting a cancerous cell displaying a candidate agent contacting a cancerous cell displaying elevated expression of a TTK-cc encoding polymuclectide with a candidate agent; and (ii) detecting the prognosis of a cancerous disease other than ovarian cancer in a contacting a cancerous disease other than ovarian cancer in a control non-cancer cell with a level of expression of the polymuclectide in the test cancer cell of a subject; and (ii) comparing a cancer cell with a level of expression of the polymuclectide in the test cancer cell with a level of expression of the polymuclectide in the test cancer cell with a level of expression of the polymuclectide in the test cancer cell with a level of expression in the control non-cancer cell is contactive to the level of expression in the control non-cancer cell is contactive of the prognosis of the cancerous disease). The methods are cancerous disease other than cancer in a subject, covarian cancer. The methods are also useful for determining the ability of a cancerous cell, identifying an agent that reduces TTK covarian cancer. The methods are also useful for determining the ability of a rational therapy. The present sequence represents a closely related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to detecting cancer (other than ovarian cancer) a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polymucleotide in a test cell obtained from the subject and in a normal polymucleotide in a test cell obtained from the subject and in a normal polymucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting cancer in a subject, by comparing expression levels of tyrosine threonine kinase polypeptide or polynucleotide in a subject cell and a normal cell, where an increase in the expression level in the test cell is indicative of cancer.
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                                                                 serine/threonine protein
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                                                      PIM-1;
                                                                                                                                                       CysGI
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                                                                                                       standard;
                                                                                                                                      GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA 1289
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                                                      protein kinase;
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                                                                                                       313
                                                      enzyme
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The present sequence is the protein sequence of the human CC serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins CC are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 CC and ABR62933) of the invention, which are therefore expected to be CC involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The CC invention relates to the use of PIM-3 nucleic acids and proteins in: CC screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus; detection assays for detecting insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, CC forensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                             New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
 Sequence 313
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Percent Similarity:
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Query Match:
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Alignment Scores: Local Similarity: Match: 7.05e-113 1670.00 100.00% 100.00% 34.87% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 313 313 0 0

US-10-705-757-1 (1-2623) x ABR62939 (1-313)

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01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                 Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                               Human Protein AAA60089, SEQ ID NO 1183.
The invention discloses a composition comprising two or more isolated rat
or human polynucleotides or a polynucleotide which represents a fragment,
                                                         New composition comprising preparing a medicament for
                                                                                                                                                                                                                                                                                                                                                                                                        29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                ADE55368
                                  Claim 1; Page; 1017pp; English
                                                                                             GENBANK; AAA60089
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CC claimed are a vector comprising the nucleic acid sequence. Also Cc claimed are a vector comprising the novel polynucleotide, a host cell Cc comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a Ck it to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying an agent CC expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a CC method for identifying a compound or small molecule that regulates the cativity in an animal of one or more of the polypetides given in the specification, a method for identifying a compound useful in treating CC pain and a pharmaceutical composition comprising the one or more composition and a pharmaceutical composition compositing the one or more compound useful in treating compound useful in treating compound useful in treating composition and a pharmaceutical composition compositing the one or more composition and apharmaceutical composition composition composition composition composition or more compound useful in treating compound useful in treating pain. Spinal segmental nerve injury (Chung), chronic constriction composition constriction will be constructed in the sequence of construction will be constructed in the sequence of construction construction will be sequence of construction will be sequence of construction will be sequenced of the printed construction of the printed construction will be constructed construction of the printed construction will be constructed construction of the printed construction will be constructed construction will be cons Sequence 313 AA; ftp.wipo.int/pub/published_pct_sequences.

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The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an
                                                                                                                                                                                                                                                                                                    Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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                                                                                                                              The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders include systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolyric anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                     Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; duillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic sclerosis; Sjogram's syndrome; vasculitis; sarcoidosis; sutcoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroi
                                                                                                    Sequence 313
                                                                                                                                                                                                                                                          Claim 7; SEQ ID NO 616; 1731pp; English.
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                                                                                                                                                                                                                                                                                                                               The present invention relates to a method of designing a ligand binding to a target molecular. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TMP receptors, G-protein coupled receptors, methyl protein. This sequence is used to illustrate the method of invention.
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16-SEP-2002;
20-SEP-2002;
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AACTTGCCGGTGGCCATCAAACACGTGGAGAAGGACCGGATTTCCGACTGGGGAGAGCTG
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coupled receptor; methyl transferase; ligase; PIM; human.
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; 2003US-0437929P.
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osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic, cantiasthmatic, hepatotropic, and respiratory activity. A polymucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its goodist, antagonist, or antibody that specifically binds to the complex through the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, control the properties, and idiopathic inflammatory myopathy, Sjogran's syndrome, systemic sclerosis, and idiopathic inflammatory myopathy, Sjogran's syndrome, systemic control thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polymeuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polymeuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary contracts of the case, an autoimmune or immune-mediated skin disease, abullous skin disease, arsthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease, abullous skin considered skin disease, as allergic rhinitis, atopic dermatitis, rejection or graft-versus-host disease. The present sequence represents a PRO protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral
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RESULT 12
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10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
                          This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine response gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of cancers, immune diseases such as allergic, autoimmune, and rheumatologic diseases, transplant rejection, and as anti-infectives for fighting viral, bacterial, parasitic and fungal infections. This sequence represents the human CR7 protein described in the invention
                                                                                                                                                                                                                                              Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR2; human; antibody; cytokine response gene; cytostatic; anti-allergic; immunosuppressive; antimicrobial; therapy; cell proliferation; treatment; cell differentiation; cancer; immune disease; rheumatologic disease; transplant rejection; anti-infective; CR7.
 Sequence 313
                                                                                                                                                                                                Example
                                                                                                                                                                                                                                                                                                                       Beadling
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GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA
                             TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a compound that modulates cell cycle arrest, useful for developing therapeutic reagents for treating cancer comprising conta a cell comprising a target polypeptide with the compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell cycle arrest; CK2-specific siRNA molecule; short interfering CK2 inhibition; PIM1-specific siRNA molecule; PIM1 inhibition; Hbo1-specific siRNA molecule; Hbo1 inhibition; cytostatic; gene th cancer; proliferative disorder; human; PIM1.
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DB; ADI57201.
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Claim 1; SEQ ID NO 22; 180pp; English.

The present invention describes a method for identifying a compound (C) that modulates cell cycle arrest. The method comprises contacting a cell comprising a target polypeptide with the compound (C), where the target polypeptide encoded by the complement of a nucleic acid that hybridises cunder stringent conditions to a nucleic acid encoding a polypeptide encoded by the complement of a nucleic acid that hybridises conditions are selected from 18 148-1408 amino acid condulating cell cycle arrest in a subject; (2) a CK2-specific short condulating cell cycle arrest in a subject; (2) a CK2-specific short contributing cell cycle arrest in a subject; (2) a CK2-specific short contributing expression of a CK2 gene in a cell; (2) a PIM1-specific siRNA molecule comprising the sequence: (II) conducted as a pairs in length; (3) inhibiting expression of a CK2 gene in a cell; (4) a PIM1-specific siRNA molecule comprising the sequence: (II) capacity (6) an Hbol-specific siRNA molecule comprising the sequence: (III) capacity (6) an Hbol-specific siRNA molecule comprising the sequence: (III) capacity (6) and conducted comprising the sequence: (III) capacity (C) has pairs in length; and (7) inhibiting expression of a PIM1 gene in a cell; (6) an Hbol-specific siRNA molecule comprising the sequence: (III) capacity (C) has pairs in length; and (7) inhibiting expression of an Hbol gene in a cell; (1) capacity (1) capacit

Sequence 313

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The invention relates to a compound targeted to a nucleic acid molecule encoding the human PIM-1 polypeptide. The compound is an antisense oligonuclectide that specifically hybridises with the nucleic acid and inhibits expression of the polypeptide. The antisense oligonucleotide comprises at least one modified internucleoside linkage i.e. a phosphorothioate linkage, at least one modified sugar moiety, preferably a 2'-O-methoxyethyl sugar moiety, or at least one modified nucleobase comprising a 5-methylcycosine. The antisense compounds are useful for modulating the expression of the human PIM-1 polypeptide and in preparation of a composition for treating hyperproliferative disorders, e.g. cancer. This sequence represents the human PIM-1 polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; PIM-1; antisense oligonucleotide; phosphorothioate 2'-O-methoxyethyl sugar moiety; 5-methylcytosine; hyperproliferative disorder; cancer; cytostatic.
                                                                                                                                                                                                                                                                                       New compound that modulates PIM-1 expression, useful in treating animal having a disease or condition, i.e. hyperproliferative dis
                                                                                                                                                                                                                                                                                                                                             WPI; 2004-374981/35
N-PSDB; ADN03035.
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Percent Similarity:
Best Local Similarity:
Query Match:
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Matches:
Conservative:
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80	61 AsnLeuProValAlaileLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80	Ф
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40	21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40	₽ b
47	411 CACGCCACCAAGCTGGCGCCCGGGAAGGAAGGAAGCCCCTGGAGTCGCAGTACCAGGTG 470	Ş
20	1 MetLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaArgAlaCysAsnAspLeu 20	DЬ
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                                        26-JAN-1999; 99US-00237543.
23-AUG-2000; 2000US-00644450.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
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                                               TGCGGGGTGCTACACGCGCGACATCAAGGACGAAAACATCCTTATCGACCTCAATCGCGGC
                                                                                                                                     GAGGAGCTGGCCCGCAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCACTGCCACAC
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                                                                                                                                                                                                                                                                             SerGlyValIleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu
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Matches:
Conservative:
Mismatches:
Indels:
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GAGATCCACCTCCACAGCCTGTCGCCGGGGCCCAGCAAA 1289 	TTCGAAGAAATCCAGAACCATCCATGGATGCAAGATGTTCTCCTGCCCCAGGAAACTGCT 1250 	TCAGAATGTCAGCATCTCATTAGATGGTGCTTGGCCCTGAGACCATCAGATAGGCCAACC 1190 	CCTTTCGAGCATGACGAAGAGATCATCAGGGGCCAGGTTTTCTTCAGGCAGAGGGTCTCT 1130 	AGGTCGGCGGCAGTCTGGTCCCTGGGGATCCTGCTGTATGATATGGTGTGGAGATATT 1070	TTCGATGGGACCCGAGTGTATAGCCCTCCAGAGTGGATCCGCTACCATCGCTACCATGGC 1010	GAGCTCAAGCTCATCGACTTCGGGTCGGGGGGCGCTCAAGGACACCGTCTACACGGAC 950

Search completed: September 22, 2005, 16:47:46 Job time: 361.494 secs

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Result

Query

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Command line parameters:

NODEL=frame+ n2p.model -DEV=xlp
-Q-(cgn2 1/USPTO gpool p/US10705757/runat 22092005 115016 22174/app query.fasta_1.5333
-DB=PublIshed applications AA -QFMT=fastam -SUPFIX=n2p.rapb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -RUD=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10705757 eCGN 11 743 @runat 22092005 115016 22174
-NCPU=6 -ICPU=3 -NO_MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPEDP=10 -YGAPEXT=0.5 -DELEXT=7
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Listing first 45 summaries
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Ygapop 10.0 , Y
Fgapop 6.0 , F
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

US-09-971-791-8

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Sequence 8, Application US/09971791

Patent No. US20020115120A1

GENERAL INFORMATION:

APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: ROSanna Kapeller-Libermann
APPLICANT: Kyle MacBeth
ITITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES
PILE REFERENCE: 35800/238856

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR FILING DATE: 1909-01-26

NUMBER OF SEQ ID NOS: 11
SOFTMARE: FastSEQ for Windows Version 4.0

LENGTH: 313
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Best Local Similarity: Query Match:
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; ORGANISM: Rattus
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                                   SerGluCysGlnHisLeuIleArgTrpCysLeuSerLeuArgProSerAspArgProSer
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APPLICANT: KORN, MARCUS
APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
FITTE OF INVENTION: PIM-3 KINASE AS A TARGET FOR
FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 12
LENGTH: 313
TYPE: PRT
ORGANISM: Rattus norvegicus
US-10-348-081-12
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APPLICANT: GRUENENTHAL GMBH
TITLE OF INVENTION: SCREENING METHOD USING PIM1-KINASE OR PIM3-KINASE
FILE REFERENCE: 029310.52018US
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PETER PETER PILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: DE 101 23 055.9
PRIOR FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: Patentin Ver: 2.1
LENGTH: 313
TYPEE: PRT
CORGANISM: Rattum norvegicum
US-10-705-757-4
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        APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
FILE REFERENCE: 35800/238856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
FRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PASC SEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRI
ORGANISM: Homo sapiens
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; Sequence 9, Application US/09971791
; Patent No. US20020115120A1
; GENERAL INFORMATION:
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APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
TITLE OF INVENTION: TTK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/081,119
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
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Publication No. US20030045491A1
GENERAL INFORMATION:
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                           GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
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APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: PRESCOLL, John C.
TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0006 US
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 52
LENGTH: 313
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US-10-394-322A-52
US-10-394-322A-52
J Sequence 52, Application US/10394322A
J Publication No. US20030232391A1
J GENERAL INFORMATION:
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           AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGGAACTG
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                                                                                             APPLICANT: KORN, Marcus
APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHAKK, Georg
TITTLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR FILE REFERENCE: DEAV2002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VETSION 3.2
SEQ ID NO 13
LENGTH: 313
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GENERAL INFORMATION:

APPLICANT: BERMER, RYAN

APPLICANT: IBRAHHM, PRABHA

APPLICANT: KUMAR, ABHINAV

APPLICANT: MUMAR, ABHINAV

APPLICANT: MILBURN, WICHAEL V.

IITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PATENTIN VET: 3.2

SEQ ID NO 1

LENGTH: 313

TYPE: PRT

ORGANISM: Homo sapiens
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        4.25e-109
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, MICHAEL V.
APPLICANT: MILBURN, MICHAEL V.
TITLE OF INVENTION; CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER: OF SEQ ID NOS: 169
SOPTWARE: PALENTIN Ver. 3.2
SEQ ID NO 150
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-664-421-150
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Best Local Similarity:
Query Match:
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US-10-664-421-150
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Sequence 9, Application US/10377268
Publication No. US20040171062A1
GENERAL INFORMATION:
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: MILBURN, MICHAEL VANCE
ITITLE OF INVENTION: METHOD FOR THE DESIGN OF
FILE REFERENCE: 039363/0303
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR PILING DATE: 2003-01-02
PRIOR PILING DATE: 2003-01-02
PRIOR PILING DATE: 2002-09-016
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTING DATE: 2002-09-20
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US-10-377-268-9
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Sequence 18, Application US/10951389
Phblication No. US2005068627A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, VIVien W.
TITLE OF INVENTION: TIK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION UMBER: US/10/951,389
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
JENGRAFI: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
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FILE REPERENCE: 16932.002

FILE REPERENCE: 16932.002

CURRENT APPLICATION NUMBER: US/10/951,406

CURRENT FILING DATE: 2004-09-27

PRIOR APPLICATION NUMBER: US/10/081,119

PRIOR APPLICATION NUMBER: 60/289,813

PRIOR FILING DATE: 2001-02-21

PRIOR FILING DATE: 2001-02-21

NUMBER: OF SEQ ID NOS: 38

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 18

SEQ ID NO 18

LENGTH: 313

TYPE: PRT

ORGANISM: Homo sapiens

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Publication No. US20050059630A1
GENERAL INFORMATION:
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in Diagnosis and
TITLE OF INVENTION: Target in Cancer
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US-10-951-477-18
; Sequence 18, Application US/10951477
; Publication No. US20050063974A1
; GENERAL INFORMATION:
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APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/951,477
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: US/10/081,119
PRIOR FILING DATE: 2002-02-21
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; PRIOR APPLICATION NUMBER: 60/289,813
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 38
; SOUTWARE: FRSTSEQ for Windows Version 4...
; SEQ ID NO 18
; SEQ ID NO 18
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-951-477-18
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                                                                                                                                     GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp
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RESULT 14
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PRIOR APPLICATION NUMBER: 10/081,119
PRIOR PILING DATE: 2002-02-21
PRIOR PELICATION NUMBER: 60/271,254
PRIOR PELICATION NUMBER: 10/360,848
PRIOR PELICATION NUMBER: 10/360,848
PRIOR PELICATION NUMBER: 09/570,593
PRIOR PELICATION NUMBER: 09/570,593
PRIOR PELICATION NUMBER: 09/570,593
PRIOR PILING DATE: 2000-05-12
PRIOR PELICATION NUMBER: 09/570,4112
PRIOR PELICATION NUMBER: 09/134,112
PRIOR PELICATION NUMBER: 10/763,692
PRIOR PELICATION NUMBER: 09/626,301
PRIOR PELICATION NUMBER: 09/626,301
PRIOR PELICATION NUMBER: 09/148,936
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PRIOR PELICATION NUMBER: 60/145,612
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Best Local Similarity:
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PRIOR FILLING DATE: 1999-05-14
PRIOR PELLICATION NUMBER: 10/763,692
PRIOR APPLICATION NUMBER: 09/626,301
PRIOR FILLING DATE: 2004-01-25
PRIOR PEPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR APPLICATION NUMBER: 60/148,936
PRIOR PILLING DATE: 1999-08-13
PRIOR PILLING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/145,612
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR PILLING DATE: 1909-07-26
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR PILLING DATE: 2003-10-30
PRIOR PILLING DATE: 2003-10-30
PRIOR PILLING DATE: 1909-07-26
PRIOR APPLICATION NUMBER: 10/698,959
PRIOR PILLING DATE: 2003-10-30
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APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
APPLICANT: Kaufmann, Joerg
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APPLICANT: Kennedy, Giulia C.
APPLICANT: Khoja, Hamiduddin
APPLICANT: Shyamala, Venkatakrishna
APPLICANT: Shyamala, Venkatakrishna
TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED IN CANCEROUS CELLS
TITLE OF INVENTION: AND THEIR METHODS OF USE V
FILE REFERENCE: 2300-21986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
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No. US20050130926A1
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RESULT 15
US-10-705-757-2
ISGUMENCE 2, Application US/10705757
Sequence 2, Application US/10705757

| Publication No. US20040146942A1
| GENERAL INFORMATION:
| APPLICANT: GRUENENTHAL GMBH
| TITLE OF INVENTION: SCREENING METHOD USING PIN
| FILE REFERENCE: 029310.52818US
| CURRENT FILING DATE: 2003-11-12
| PRIOR APPLICATION NUMBER: US/10/705,757
| PRIOR FILING DATE: 2002-05-13
| PRIOR FILING DATE: 2002-05-13
| PRIOR FILING DATE: 2001-05-11
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; SOFTWARE: PatentIn Ver.
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
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Search Job ti	B	Ś	₽	Ş
Search completed: September 22, 2005, 17:46:43 Job time : 184.828 secs	301 GluileHieLeuHisSerLeuSerProGlyProSerLys 313	904 GAGATTCATCTGCACAGCCTGTCACCATCACCCAGCAAA 942	281 PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla 300	844 TITGAAGAAATCCAGACCATCCGTGGATGCAGGATGTTCTCCTGCCCCAGGCCACCGCC 903

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-Qx/cgn2 1/USPTO_spool_p/US10705757/runat_22092005_115015_22129/app_query.fasta_1.5333
-Qx/cgn2 1/USPTO_spool_p/US10705757/runat_22092005_115015_22129/app_query.fasta_1.5333
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -L\OOPEL=0 -L\OOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCGALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pco -NORM=ext -HRAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757 @CGN 1 1 980 @runat 22092005_115015_22129 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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     GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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PIM1_FELCA
PIM1_HUMAN
PIM1_BOVIN
PIM3 XENLA
Q8R2P0
PIM2 MOUSE
PIM2 HUMAN
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PIM3_COTJA
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Q91822
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	Q6ckw4 kluyveromyc	O61298 halocynthia	Q6frs7 candida gla			Q9w532 drosophila		Q38997 arabidopsis	m mu	O60285 homo sapien		Q6c310 yarrowia li			glyc		mus I	cani		Q6p2j9 homo sapien	Q17737 caenorhabdi	Q8t3f1 caenorhabdi	-		Q6di52 brachydanio			

ALIGNMENTS

PIMI RAT

ID PIMI RAT

ID PIMI RAT

ID PIMI RAT

AC P26793;

DT 01-NUG-1992 (Rel. 23, Last sequence update)

DT 01-NUG-1992 (Rel. 23, Last sequence update)

DT 01-NUG-1992 (Rel. 24, Last annotation update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Proto-oncogene serine/threonine-protein kinase Pim-1 (BC 2.7.1.37).

Rattus norregicus (Rat).

OS Rattus norregicus (Rat).

OS Rattus norregicus (Rat).

OX NCBI TaxID=10116;

RN SEQUENCE FROM N.A.

RE STRAIN-Sprague-Dawley, TISSUB=Testis;

RA WINGEL TaxID=10116;

RE SEQUENCE FROM N.A.

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PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00110; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

R PROSITE; PS00108; PROTEIN KINASE.

PROTEIN KINASE.

PROTEIN KINASE.

PROTEIN KINASE.

R PROSITE; 167 ATP (By similarity).

R PRINDING 67 ATP (By similarity).

PROTEIN SITE 167 167 PROTON acceptor (By sim: SEQUENCE 313 AA; 35630 MW; D5757DA9F1821BF9 CRC6.
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                                                                                                                 GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp
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                                AGGTCGGCTGCTTTGGTCCCTGGGGATCCCTGCTCTATGACATGGTCTGCGGAGATATT
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Best Local Si Query Match: DB:

Percent Similarity:

Similarity:

1.41e-97 1638.00 98.72% 97.44% 67.05%

Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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Q95LJ0;
28-FEB-2003
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-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By -!- PTM: Autophosphorylated (By similarity).
                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                               ATP-binding, Nuclear protein, Phosphorylation, Serine/threonine-protein kinase, Transferase.
                                                                                        PRODOM; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1
PROSITE; PS50011; PROTEIN KINASE DOM; 1
PROSITE; PS00108; PROTEIN KINASE ST; 1.
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InterPro; IPR011009; Kinase like.
InterPro; IPR0007719; rot kinase.
InterPro; IPR008271; Ser thr pkin
Dfam: PF00069: Pkinase: 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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ProDom; PD000001
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RESULT 3
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   RX MEDLINE=2238/257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rahey J., Helton E., Ketteman M., Wadan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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MEDLINE-90382681; PubMed=22
Reeves R., Spies G.A., Kief
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Gene 90:303-307(1990).
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MEDLINE=88246418; PubMed=2837645; Telerman A., Amson R., Zakut-Houri R., Givol D.; "Identification of the human pim-1 gene product cytoplasmic protein with tyrosine kinase activit mol. Cell. Biol. 8:1498-1503(1988).
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MEDLINE=22388257;
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"Cloning and characterization of the human
oncogene related to the protein kinases.",
J. Cell. Biochem. 35:105-112(1987).
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"The cDNA sequence and
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MEDLINE=88115604; PubMed=3429489;
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dern M., Hermans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2205533; I
G.A., Kiefer M., I
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Primates;
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Barr P.J., Power M.;
e human oncogene, pim-1.";
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A Ionov Y., Le X., Tunquist B.J., Sweetenham J., Sachs T., Ryder J.,

A Johnson T., Lilly M.B., Kraft A.S.;

Tohnson T., Lilly M.B., Kraft A.S.;

In Johnson T., Lilly M.B., Kraft A.S.;

In The protein kinase is nuclear in Burkitt's lymphoma: nuclear

In Incalization is necessary for its biologic effects.";

Anticancer Res. 23:167-178(2003).

In Lanticancer Res. 23:167-178(2003).

C -!- FUNCTION: Thought to play a role in signal transduction in blood cells. May affect the structure or silencing of chromatin by phosphorylating HP1 gamma/CBX3.

C -!- FUNCTION: Thought to PR9 (By similarity).

C -!- SUBUNIT: Binds to RP9 (By similarity).

C -!- SUBUNIT: Binds to RP9 (By similarity) in cells of the hematopoletic and germ line lineages.

C -!- FINSIDE SPECIFICITY: Expressed primarily in cells of the hematopoletic and germ line lineages.

C -!- FINI Autophosphorylated on tyrosine residues.

C -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                       R GO; GO:0005/37; C:cytoplasm; TAS.
R GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
GO; GO:0007275; P:development; TAS.
R GO; GO:0007275; P:development; TAS.
R InterPro; IPR001009; Kinase like.
R InterPro; IPR001009; Kinase like.
R InterPro; IPR000719; Prot kinase.
R InterPro; IPR0008271; Ser Thr pkin_AS.
R Pfam; PP00069; Pkinase; 1.
R Pfam; PP00069; Pkinase; 1.
R PF0Dy; PP0000001; PROTEIN KINASE DOW; 1.
R PROSITE; PS00107; PROTEIN KINASE DOW; 1.
R PROSITE; PS00108; PROTEIN KINASE DOW; 1.
R PROSITE; PS00108; PROTEIN KINASE ST; 1.
R PROSITE; PS00108; PROTEIN KINASE TOW; 1.
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EMBL; M16750; AAA60089.1; -.
EMBL; M54915; AAA3647.1; -.
EMBL; M24779; AAA81553.1; -.
EMBL; BC020224; AAH20224.1; -.
EMBL; AF386792; AAK70871.1; -.
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DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/PIMIID261.html"
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PIM1_BOVIN

RESULT 4

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Percent Similarity:
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ProDom; PD000001; Prot_kinase; 1.

PROSITE; PS00100; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

*""-hinding; Nuclear protein; Phosphorylation; Protein kinase; Transferase.

*""-hinding; Nuclear protein kinase; Transferase.
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Eukaryota; Metazoa; C
Mammalla; Eutheria; C
Bovinae; Bos.
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28-FEB-2003
05-JUL-2004
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-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- PTM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM subfamily.
                                                                                                                                                                                                                                                                                                                                      EMBL; AP259078; AAF67200.1; -.
HSSP; Q63450; 1A06.
InterPro; IPR011009; Kinase like.
InterPro; IPR00719; Prot_kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
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167
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(Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
ene serine/threonine-protein kinase
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38 290
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ATP (By similarity).
ATP (By similarity).
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Proton acceptor CRy s
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Conservative:
Mismatches:
Indels:
Gaps:
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Mammalia; Eutheria;
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RESULT RE
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QBCCN8;
O1-MAR-2003 (TrEMBLrel. 23, C:
O1-MAR-2003 (TrEMBLrel. 23, L:
25-OCT-2004 (TrEMBLrel. 28, L:
Proviral integration site 1.
Name=Piml;
SEQUENCE FROM N.A.

STRAIN=C57BL/6; TISSUE=Brain, and Eye;

MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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theria; Rodentia;
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EMBL; BC042885; 1
EMBL; BC053019; 1
EMBL; BC055316; 1
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PMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; 1

ATP-binding; Kinase; Serine/threonine-protein kinase; 1

ATP-binding; Kinase; Serine/threonine-protein kinase; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:97584; Piml.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:00046774; F:protein serine/threonine kinase activity;
GO; GO:00046774; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPRO1009; Kinase like.
InterPro; IPRO10719; Prot kinase.
InterPro; IPRO102290; Ser thr Dkinase.
InterPro; IPRO02291; Ser thr Dkinase.
InterPro; IPRO02290; Ser thr Dkinase.
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STRAIN=C57BL/6; TISSUE=Brain;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted JUL-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (JAN-2003)
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"Generation and initial analysis of more than 15,000 full-length and mouse cDNA sequences";
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6;
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                                                                             CACGCCAACAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG
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HisalaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal
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; AAH53019.1; -.
; AAH55316.1; -.
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MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
Domen J., van Beveren C., Berns A.;
"The primary structure of the putative oncogene pim-1 shows extensi
                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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MEDLINE-20389540; PubMed-10931201;
MALTA H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
"PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
EUR. J. Biochem. 267:5168-5178(2000).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Binds to Rep.
-!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
-!- PTM: Autophosphorylated (By similarity) activated by provirus insertion in murine leukemia virus-induced T-cell lymphomas.
-!- SUMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
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MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355; Bichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.; "Developmental expression of Pim kinases suggests functions also outside of the hematopoietic system."; Oncogene 19:1215-1224(2000).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote:
-!- PTM: Autophosphorylated.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. I subfamily.
                                                                                                                                                                                                                                                       Name=PIM3; Synonyms=PIM-3;
Coturnix coturnix japonica (Japanese quail).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
Serine/threonine-protein kinase Pim-3 (EC 2
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InterPro; IPRO01719; Prot kinase.
InterPro; IPRO02290; Ser_thr_pkinase.
InterPro; IPRO08271; InterProperty interProper
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ATP (By similarity).
Proton acceptor (By similarity);
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PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6;

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Mammalia; Eutheria;
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29-MAR-2004 (Rel. 43, Last sequence update)
05-UL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
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IDENTIFICATION FROM MEDLINE=22682943; Pu
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InterPro; IPR011009; Kinase 11ke.
InterPro; IPR001719; Prot kīnase.
InterPro; IPR00271; Ser thr pkin_AS.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTĒIN KINASE ATP; 1.
PROSITE; PS00107; PROTĒIN KINASE DOW; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Phosphorylation; Serine/threonine-protein kinase;
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-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosp -i- SIMILARITY: Belongs to the Ser/Thr protein kinase f
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RC STRAIN-FVB/N, TISSUS-Colon, and Salivary gland;
RX MEDLINE-22388257; pubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L. H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., McEwan R.J., Malek J.A., Gunaratne P.H.,
RA Raha S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards J., Wolng A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
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"T "Generation and initial analysis of more than 15,000 full-length human
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation updat
Serine/threonine-protein kinase Pim-3 (EC 2
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Mammalia; Eutheria;
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InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR008279; Ser thr pkin AS.
InterPro; IPR002290; Ser thr pkinase.
Pfam; PF00069; Pkinase; 1.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKG; 1.
SMART; SM00220; S TKG; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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InterPro; IPR011009;
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                                                     TTCGTGCTGATCCTGGAGAGGCCCGAACCCGTGCAAGACCTCTTCGACTTCATCACCGAG
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                               MetLeuLeuSerLysPheGlySerLeuAlaHisLeu---CysGlyProGlyGlyValAsp
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
CDD68CBF46354851E CRC64;
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Mismatches:
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IM3_RAT
ID PIM3_RAT
ID PO1444;
AC O70444;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Pim-3 (EC 2.7.1

Kid-1) (Kinase induced by depolarization).

"""" (Rat).

""" (Rat).

""" (Rat).

""" (Primalata; Verte
  SEQUENCE FROM N.A., AND CHARACTERIZATION.

MEDLINE=98298176; PubMed=9623723; DOI=10.1074/jbc.273.26.16535;

Feldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,

Bazan N.G., Baudry M., Herschman H.R.;

"KID-1, a protein kinase induced by depolarization in brain.";

"KID-1, a protein kinase induced by depolarization in brain.";

J. Biol. Chem. 273:16535-16543 (1998).

-i- TISSUE SPECIFICITY: Present in a number of unstimulated tissue in the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Konietzko U., Kuhl D.;
"Pim-3 is a member of the pim kinase family.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
[2]
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isb-or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                            including brain.
-!- INDUCTION: By membrane de-
-!- PTM: Autophosphorylated
-!- SIMILARITY: Belongs to t
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Sciurognathi; Muridae; Murinae; Rattus.
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R InterPro; IPR000719; Prot Kinase.

R InterPro; IPR000719; Ser_thr_pkin_AS.

R InterPro; IPR002290; Ser_thr_pkinase.

R InterPro; IPR002290; Ser_thr_pkinase.

R Pfam; PP00069; Pkinase; I.

R ProDom; PD000001; Prot kinase; 1.

R ProDom; PD000001; Prot kinase; 1.

R SMART; SM00220; S_TKc; 1.

R PROSITE; PS00107; PROTEIN KINASE ATP; 1.

R PROSITE; PS001108; PROTEIN KINASE_ST; 1.

ATP-binding; Phosphorylation; Serine/threonine-protein kir
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EMBL; AP057026; AAC36065.1; --
HSSP; Q03656; 1HOW.
RGD; 620462; Pim3.
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ATP (By similarity).
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
; DD6C9BF4635F851E CRC64;
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Matches:
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Alignment
Pred. No.:
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DB:
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                                                                                                           Percent Similarity:
Best Local Similarity:
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RGD; GO:0005524; F:ATP binding; IEA.

RGO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0004668; P:protein amino acid phosphorylation; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR011009; Kinase like.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR008271; Ser Thr_pkin_AS.

PFam; PF00069; Pkinase; I.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS0011; PROTEIN KINASE_ST; 1.

DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
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Q811X8;
Q1-JUN-2003
Q1-JUN-2003
Q1-MAR-2004
                                                                                                                                                                                                                                                             MGD; MGD; MGD; GO; GO; GO
                                                                                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ c-i- SIMILARITY: Belongs to the Ser/Thr protein EMBL, AY026239; AXX16606.1; -. HSSP; Q03656; 1Q99.
                                                                                                                                                                                                                                                                                                                                                                                 Name=Pim3; Synonyms=Kid1;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Roden
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                  Match:
                                                                                                                                       Мо.:
                                                                                                                                                Scores:
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GACCTGCACGCCAACAAGCTGGCGCCCCAAA----GAGAAGGAGCCCCCTGGAGTCGCAG
                                 (1-1302)
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Rodentia;
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Last sequence update)
Last annotation update)
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TISSUE=Embryo;

PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler

Klausner R.D., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.
                                                                                                                          SEQUENCE
TISSUE=Em
                                                                                                                                                                                                                           Q66III PRELIMINARY; PRT; 318 AA.
Q66III;
Q66III;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Created)
26-OCT-2004 (TrEMBLrel. 28, Last sequence update)
27-OCT-2004 (TrEMBLrel. 28, Last sequence update)
28-OCT-2004 (TrEMBLrel. 28, La
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SerGluArgProSerLeuAspLysLeu---CysH1sProTrpMet
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TyrGlnValGlyAlaValLeuGlySerGlyGlyPheGlyThrValTyrAlaGlySerArg
                                                                                                                                                    FROM N.A.
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A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Willalon D.K., Muzny D.M., Sodergren B.J., Lux., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lux., Gibbs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Holdstein M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
A Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Tand mouse cDNA sequences.";
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SMART; SM00210; TYCK; 1.

SMART; SM00219; TYCKC; 1.

SMO0219; TYCKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1

PROSITE; PS00101; PROTEIN KINASE DOM; 1

PROSITE; PS00108; PROTEIN KINASE_ST; 1.

Hypothetical protein.

SEQUENCE 318 AA; 36547 MW; 48CCF127;
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Submitted (AUG-2004) to the EMBL/GenBar EMBL; BC081340; AAH81340.1; ...

InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot kInase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkin AS.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF00069; Pkinase; I.
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GAACTGCCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCG
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                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M.
Aebersold R., Pelech S.L.;
"Identification of the autophosphorylation sites of the Xenopus
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) serine/threenine-protein kinase Pim-3 (EC
                                                                                                                                                                                                                                                                                                                                                                                                               Q91822;
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                   Name-PIM3; Synonyms-PIM1;
Kenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                 NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998
                                                                                                                                                                                                     Biol.
                                                                                                                subfamily.
CAUTION: Was originally (Ref.1)
represent the pim-3 isoform.
                                                                                                                                                                                    -1 proto-oncogene-encoded protein kinase.";
Biol. Chem. 272:10514-10521(1997).
CATALYTIC ACTIVITY; ATP + a protein = ADP
                                                                                                                                                            PTM: Autophosphorylated.
SIMILARITY: Belongs to the Ser/Thr protein kinase
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ProDom; PD000001; Prot kinase; I.

PROSITE; PS00107; PROTEIN KINASE ATP;

PROSITE; PS00101; PROTEIN KINASE DOM;

PROSITE; PS00108; PROTEIN KINASE ST;

PROSITE; PS00108; PROTEIN KINASE ST;
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ATP-binding;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser fhr pkin
InterPro; PR00869: Pkinase; I.
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LysValProThrAlaPheArgGlyValIleAsnLeuLeuAspTrpTyrGluArgProAsp
GACACAGTCTACACGGACTTTGACGGAACCCGAGTGTACAGTCCTCCAGAGTGGATTCGC
                                     :::|||
ValAspThrArgAsnGlyGluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLys
                                                ATCGACCTGAACCGCGGCGAACTCAAACTCATCGACTTCGGGTCGGGGGGCGCTGCTCAAG
                                                                                 GTGCGGCATTGCCACAACTGCGGGGGTTCTCCCACCGCGACATCAAGGACGAGAACATCTTA
                                                                                                                                  TCCGACTGGGGGGAACTGCCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAG
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ThrGluTrpGlyThrLeu---AsnGlyValMetValProLeuGluIleValLeuLeuLys
                                                                                                                                                                                                                                                                                                                                  AspSerArgIleAlaAspGlyGlnProValAlaValLysHisValAlaLysGluArgVal
                                                                                                                                                                                                                                                                                                                                                    GGCATCCGCCGACAACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATT
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ATP (By similarity).
Proton acceptor (By similarity).
Phosphoserine (by autocatalysis)
(partial)
Phosphoserine (by autocatalysis).
Phosphothreonine (by autocatalysis)
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ATP (By
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RM MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2238857; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Alusner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RX Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RX Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RX Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Altaschin M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RX Altaschin M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RX Altaschin M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

RX Altaschin M.J., Medlan N.B., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Altaschin S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RX Allalon D.K., Modan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Bouffard G.G.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Bouffard G.G.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Bouffard G.G.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Schein J.E.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y., Shein J.S.,

RX Allalon D.K., Toung A.C., Shevchenko Y.,
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01-JUN-2002
01-JUN-2002
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
-I- SIMILARITY: Belongs to the Ser/Thr protein kinase famil; GBMBL; BC027376; AAH27376.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
                                                                                                                                       Strausberg R.;
Submitted (APR-2002) to
                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary
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l. Acad. Sci. U.S.
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InterPro; IPR0010719; Prot Kinase.
InterPro; IPR0010719; Prot Kinase.
InterPro; IPR0010719; Ser thr Dkinase.
InterPro; IPR001071; Ser thr Dkinase.
InterPro; IPR001071; Ser thr Dkinase.
InterPro; IPR001071; Ser thr Dkinase; 1.
SYNORT; SM00107; PROTEIN_KINASE ATP; 1.
SYNORTS; PS00107; PROTEIN_KINASE DAM; 1.
PROSITE; PS00108; PROTEIN_KINASE DAM; 1.
PROSITE; PS00108; PROTEIN_KINASE DAM; 1.
PROSITE; PS00108; PROTEIN_KINASE DAM; 1.
SPROSITE; PS00108; PROTEIN_KINASE DAM; 1.
SPROSITE; PS00108; PROTEIN_KINASE DAM; 1.
STP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 311 AA; 34486 MM; F7B770908D23A710 CRC64;
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yLysAsgArgAlaAlaPheGluAlaGluTyrArgLeuGlyProLeuLeuGlyLysGlyGl
                            AGAGATCGTCAAGGGCCAAGTGTACTTTAGGCAAAGGGTCTCTTCAGAATGTCAACATCT
                                                                       CGACATCAAGGACGAGAACATCTTAATCGACCTGAACCGCGGGGAACTCAAACTCATCGA
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222 740 242 800 182

142 500 162 266

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R HSSP; 063450; laub.

R HSSP; 0637587; pim2.

R GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0004674; F:protein serine/threonine kinase activity;

GO; GO:0006916; P:anti-apoptosis; IDA.

DR GO; GO:0006917; P:apoptotic mitochondrial changes; IDA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkinase.

DR InterPro; IPR008271; Ser_thr_pkinase.

DR Ffam; PP00069; Pkinase; I.

DR PROSITE; PS001001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

PROSITE; PS00101; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                      PIMSULT 15
PIMSULT 28-PEB
DT 28-PEB
DT 28-PEB
DT 28-PEB
DT SE-PEB
DT S
                                                                                                                                                                                                                                                                                                                            EMBL; L41495; AAA98922.1; -.
EMBL; L41495; AAA98923.1; -.
EMBL; L41495; AAA98924.1; -.
EMBL; L41495; AAA98924.1; -.
PIR; S55333; S55333.
HSSP; Q63450; IA06.
MGD; MGD: 97587; Pim2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-95300786; PubMed-7781606; Verhoeven E., Linders van der Lugt N.M., Domen J., Verhoeven E., Linders van der Gulden H., Allen J., Berns A.; "Proviral tagging in E mu-myc transgenic mice lacki oncogene leads to compensatory activation of Pim-2. EMBO J. 14:2536-2544 (1995).

-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q62070; Q62071; Q62072;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Pim-2 (EC 2.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa,
Mammalia, Eutheria,
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Pim2; Synonyms=Pim-2;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BIM2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS:
Event-Alternative initiation;
Comment-3 isoforms, 1 (shown here), 2
alternative initiation. Isoform 1 and
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||||||||||||||||||||
pPheGlySerGlyAlaLeuLeuHisAspGluProTyrThrAspPheAspGlyThrArgVa
                                                                                                                                                                                                                                                                                                            CGACATCAAGGACGAGAACATCTTAATCGACCTGAACCGCGGGGGAACTCAAACTCATCGA
                                                                                                                                                                                                                                                                                                                                                                GTACAGTCCTCCAGAGTGGATTCGCTACCATCGCTACCACGGCAGGTCGGCTGCTGTTTG
                                                                                                                                                                                                                                                                                       gAspIleLysAspGluAsnIleLeuIleAspLeuCysArgGlySerIleLysLeuIleAs
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yPheGlyThrValPheAlaGlyHisArgValThrAspArgArgGlnValAlaIleLysVa
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity);
; 12BB70BFD04DBE8A CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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740 301

281 680 261 620 560

221 500 201 440

241

181

380 161 320 141

266 121 206 5 146

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Command line parameters:

MODEL-frame+ n2p.model -DEV=xlp
-Q-(cgn2_1/USFTO_8pool_p/US10705757/runat_22092005_115016_22154/app_query.fasta_1.5333
-DB=Issued_Patents AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=51ts -START=1 -END=-1 -MARTIX=b10sum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10705757 @CGN 1 1 137 @runat 22092005 115016_22154 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NGE_SCORES=0 -MAIT -DSPEIOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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      seq length:
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Ygapop 10.0 , Ygapext
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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ALIGNMENTS

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Sequence 8, Application US/09237543A
PATENT NO. 6143540
GENERAL INFORMATION:
APPLICANT: KADELIEY, ROBANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE HR
TITLE OF INVENTION: AND USES THEREOP
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
CURRENT FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                       US-10-705-757-3 (1-1302) x US-09-237-543-8 (1-313)
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TYPE: PRT
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; FILE REFERENCE
Sequence 8, Application US/09644450
PAtent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 313
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Sequence 9, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:
APPLICANT: Kapeller, ROBANA

TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TITLE OF INVENTION: AND USES THEREOF
PILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT PILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 9

LENGTH: 313

TYPE: PRT
ORGANISM: Homo Bapiens

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Query Match:
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SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo s
US-09-644-450-9
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APPLICANT: KAPELIEV, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF TH
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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                     CCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGCTTC
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RESULT 5
US-08-463-081B-26
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FITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
FITLE OF INVENTION: Vector and Transformed Cell Thereof, and Ex
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
STREET: 444 South Flower St. - Suite 1900
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPITTED
                                                                                                                                                                                                                                                                  Sequence 26, Application US/08463081B Patent No. 5871960 Patent No. 5871960 5837487
                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Smith,
APPLICATION NUMBER: US/08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: US 08/104,736
PILING DATE: 10-AUG-1993
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Pred. No.:
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APPLICATION UNMBER: US 07/796,0
EILING DATE: 20.NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
NOLECULE TYPE: peptide
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RESULT 6
US-08-461-379A-26
Sequence 26, Application US/08461379A
Patent No. 5871961
GENERAL INFORMATION: Nucleic Acids Encoding CRS Polype
TITLE OF INVENTION: Nucleic Acids Encoding CRS Polype
TITLE OF INVENTION: Nucleic Acids Encoding CRS Polype
TITLE OF INVENTION: Expression Thereof
NUMBER OP SEQUENCES: 35
CORRESSEE: Ratner & Prestia
ADDRESSEE: Bennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Patentin Release #1.0,
SOFTWARE: PATENTIN NUMBER: USA
FILING DATE: 5-UNE-195
PRIOR APPLICATION NUMBER: USA
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RESULT 7
US-08-462-390B-26
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; Patent No. 58828
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          Sequence 26, Application Patent No. 5882894
GENERAL INFORMATION:
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FILING DATE: 27-CCT-1994
APPLICATION UMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: J0,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (610)407-0701 INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPOTER:
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Transform
NUMBER OF SEQUENCES; 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
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LENGTH: 313 amino acid
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FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
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                                             AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGAACTG
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PATENT NO. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRI
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-UN-1995
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION UMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: Patentin Release #1.0,

SOPTWARE: Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 90071
                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301
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. (B) STREET:
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: pepti
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                                                                                 AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGGAACTG
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CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly
                                                                                                                                      TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAACCGCGGC
                                                                                                                                                                                           GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC
                                                                                                                                                                                                                GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
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66.43%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 26, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Pol
TITLE OF INVENTION: Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSEE: (B) STREET:
CITY: Los Angeles
STRIE: Californiaa
                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-08-465-585C-26
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 US-10-705-757-3
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SOFTWARE: PATENTIN DATA:
APPLICATION UNMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
PILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38149 (DATELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                             TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COUNTRY: US;
ZIP: 900071
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RESULT 10
US-08-652-446-26
Sequence 26, Application US/08652446

Sequence 26, Application US/08652446

PATENT NO. 6057427

PATENTION: GENERAL INFORMATION: Applicant: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR5

TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell TITLE OF INVENTION: Expression Thereof
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Version #1.25
CURRENT APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JUN-1996
PRIOR APPLICATION NUMBER: US/08/652,446
FILING DATE: 5-JUN-1996
PRIOR APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION NUMBER: US 08/330,108
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/461,379
PRIOR APPLICATION NUMBER: 08/462,380
PRIOR APPLICATION NUMBER:
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Best Local Similarity:
Query Match:
                                           US-10-705-757-3 (1-1302) x US-08-652-446-26 (1-313)
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RESULT 11

US-09-237-543-7

US-09-237-543-7

Sequence 7, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HK
TITLE OF INVENTION: AND USES THEREOF
PILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,543A
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NUMBER OF SEQ ID NOS: 11

SOFTWARE: PATENTIN Ver. 2.0

SEQ ID NO 7

LENGTH: 313

TYPE: PRT

ORGANISM: Mis musculus
US-09-237-543-7
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                                               AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGGAACTG
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Percent Similarity:
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Query Match:
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-644-450-7
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US-09-644-450-7
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Patent No. 6381791
GENERAL INFORMATION:
APPLICANT: Kapeller, ROBANA
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035809/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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                                                GluAspLeuAlaArgGlyPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn
                                                                GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC
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APPLICANT: Benner
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                                                                                                MOLECULE TYPE:
DESCRIPTION:
ORIGINAL SOURCE:
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OPERATING SYSTEM: MacIntosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Benner, TITLE OF INVENTION:
                                                                    FEATURE: Protein kinase; Table 8 Column
                                                     PUBLICATION INFORMATION:
   AUTHORS:
AUTHORS:
AUTHORS:
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CITY: Z
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CLASSIFICATION: 436
                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
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; AUTHORS: Hunter T.
; TITLE: The protein kinase f:
; JOURNAL: Science
; VOLUME: 241
; PAGES: 42-52
; DATE: 1988
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                              TTTAGGCAAAGGGTCTCTTCAGAATGTCAACATCTTATTAGATGGTGCCCTGTCCCCTGAGA
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; GENERAL INFORMATION: ADBLICANT: KAPPLICANT: KAPPLICANT: KAPPLICANT: MAPPLICANT: NOVEL MOLECULES OF THE HKID-1-RELATED PROFITIE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROFITIE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,543A
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS; 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo Bapiens
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APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 326
TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Kapeller
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Search completed: September 22, 2005, 17:24:35 Job time : 42.242 secs

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-Q-/cgn2_1/USPTO_spool_p/US10705757/runat_22092005_115014_22122/app_query.fasta_1.5333
-DB=A_Geneseq_-OFMT=fastan_-SUFTX=n2p.rag_-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=blte -START=1 -ENDE-1 -MATRIX+blosum62 -TRANS=human40.cdi -LIST=45
-DCGALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTEMT=pto -NORM=ext -HBAPSIZE=550 -MINLENS - MAXLEN=200000000
-USER=US10705757 @CGN 1 1_753 @runat_22092005_115014_22122 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LOGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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ALIGNMENTS

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DT 20-DEC-2002 (first entry)
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Rattus norvegicus.

N US2002115120-A1.

PD 22-AUG-2002.

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F 04-OCT-2001; 2001US-00971791

PR 26-JAN-1999; 99US-00237543. PR 23-AUG-2000; 2000US-00644450.

PA (MILL-) MILLENNIUM PHARM INC

I Kapeller-Libermann R, Rudolph-Owen LA, Macbeth

WPI; 2002-712471/77.

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of modulating the level or a human HKID-1 polypeptide, a member of serine/threonine kinase
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                                                                                                                                                                                            Sequence 313
                                                                                                                                                                                                                                                               The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human or murine PIM-3 DNAs or polypeptides, useful for agent for identifying anti-type 2 diabetes mellitus drugs, treating insulin resistance or type 2 diabetes mellitus.
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N-PSDB; ABV73989.
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The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method useful for modulating the level or activity of HKID-1 polypeptide or polypeptide or activity of HKID-1 polypeptide or polypeptide or activity of HKID-1 polypeptide or polypeptide or method useful for modulating the level or activity of HKID-1 polypeptide or polypeptide or polypeptide or polypeptide or predisposed to having a disorder
                                                                                                                                                                      Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoletic neoplastic disorder; Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML; Waldenstrom's macroglobulinaemia; WM; human.
                                                                                                                                                                                                                                                                                                                                                     26-JAN-1999;
23-AUG-2000;
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                                                                                                                                           Example 3;
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involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous leukaemia (CML) and Waldenstrom's macroglobulinaemia (WM). This is the amino acid sequence of a human protein kinase phosphorylation site

(1-313)Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 304 304 0

AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGGAACTG HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal CACGCCAACAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG ATGCTCTTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCAGCCCCTTGCAACGACCTG AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80 243 60 183 40 20

TCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTG LeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu 120 100

GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln 140 423

GAGGAGCTGGCCCGGAGCTTCTTCTGGCAGGTGCTGGAGGCCGTGCGGGATTGCCACAAC

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180

TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAACCGCGGC CysGiyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly

GAACTCAAACTCATCGACTTCGGGTCGGGGGGCGCTGCTCAAGGACACAGTCTACACGGAC

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                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with pIMI or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or neurodegenerative diseases). The present sequence is human PIM1 kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for identifying analgesics, useful particularly for treating chronic pain, by screening compounds for interaction with PIM-1 or kinase, or related compounds.
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                                                                                                                                                                                                                                                                                 CC non-cancer cell, where an increase in the expression level of TTK protein CC indicates the presence of cancer other than ovarian cancer. Also included CC are reducing growth of a cancerous cell (by contacting a cancerous cell CC in the cell), an assay for identifying a candidate agent that reduces CC growth of a cancerous cell (comprising: (i) detecting the activity of a CTK polypeptide in the presence of a candidate agent; and (ii) comparing CC the activity of TTK polypeptide activity in the absence of the candidate agent contacting a cancerous cell (comprising: (i) detecting the activity of a CTK polypeptide in the presence of a candidate agent; and (ii) comparing CC the activity of TTK polypeptide activity in the absence of the candidate agent contacting a cancerous cell displaying elevated expression of TTK-condidate agent that reduces TTK activity) and assessing the prognosis of a cancerous disease other than ovarian cancer in a contacting polynucleotide with a candidate agent; and (ii) determining the cell of expression of TTK-encoding polynucleotide in a test cancer cell of a subject; and (ii) comparing a CC level of expression of TTK-encoding polynucleotide in a test cancer cell of a subject; and (ii) comparing a CC level of expression of TTK-encoding polynucleotide in the test cancer cell with a level of expression of TTK in the test cancer cell with a level of expression of TTK in the test cancer cell is indicative of the prognosis of the polynucleotide in a control non-cancer cell is contactive to the level of expression in the control non-cancer cell is concerned to the prognosis of the cancerous disease other than cancer. The methods are also useful for determining the ability of a cancerous disease other than cancer. The methods are also useful for determining the ability of a cancerous disease other than covarian cancer. The methods are also useful for determining the ability of a cancerous disease. The ability of a cancerous disease other than covarian cancer than ability of a cancerous disea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting cancer in a subject, by comparing expression levels of tyrosine threonine kinase polypeptide or polynucleotide in a subject cell and a normal cell, where an increase in the expression level in the test cell
                                                                                                                                                                                                                                                            Sequence 313
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C screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, corresponded by predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type 2 diabetes medicine to the treatment of insulin resistance or type 2 diabetes medicament for the treatment of insulin resistance or type 2 diabetes medicament for the treatment of insulin resistance or type 2 diabetes medicament for the treatment of insulin resistance or type 2 diabetes medicament for the treatment of insulin resistance or type 2 diabetes medicament for the treatment of insulin resistance or type 2
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spinal segmental nerve injury; chronic constriction injury; CCI;
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                                           GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
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                                                                       Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
                                                  Disclosure;
                                                                                                                                                             Prescott JC,
                                                                                                                                                                                                               21-MAR-2002; 2002US-0366892P
                                                                                                                                                                                                                                       20-MAR-2003; 2003WO-US008725
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The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). T method involves contacting inactive conformation of (T), which contains

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                                                                              The invention relates to human PRO polypeptides and the polynucleotides encoding them. The polypeptides and polynucleotides are useful for treating and diagnosing immune related disorders in mammals. The immune related disorders in chide systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, systemic sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central or peripheral nervous system, demyelinating polyneuropathy, Guillain-Barre syndrome and chronic inflammatory demyelinating polyneuropathy. This sequence represents a human PRO polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; PRO; immune related disorder; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis; systemic solerosis; Sjogren's syndrome; vasculitis; sarcoidosis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis; diabetes mellitus; renal disease; demyelinating disease; central nervous system; peripheral nervous system; demyelinating polyneuropathy; Guillain-Barre syndrome; chronic inflammatory demyelinating polyneuropathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or spondyloarthropathy.
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Molecular
G-protein
                     The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TMF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the human PIM 1 protein. This sequence is used to illustrate the method of invention.
                                                                                                                                                                                           Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand
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16-SEP-2002; 2002US-0411398P.
20-SEP-2002; 2002US-0412341P.
02-JAN-2003; 2003US-0437929P.
                                                                                                                                                                  Disclosure; SEQ ID NO 9; 186pp; English.
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  01-NOV-2002; 2002US-0423394P
                                             30-OCT-2003; 2003WO-US034312.
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CC antiasthmatic, and respiratory activity. A polynuclectide CC of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the CC agonist, antagonist, or antibody that specifically binds to the CC golypeptide is useful for treating an immune related disorder such as CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, cyteoarthritis, as spondyloarthropatthy, systemic sclerosis, and idiopathic inflammatory myopathy, Sjogren's syndrome, systemic celerosis, and cidiopathic inflammatory myopathy, Sjogren's syndrome, systemic sclerosis, and cidiopathic marcoidosis, autoimmune haemolytic anaemia, autoimmune charmolytic anaemia, a hepatobiliary cirrhosis, granulomatous hepatitis, Gulilain-Barre syndrome, confisease, infectious or autoimmune chronic active hepatitis, primary confisease, infectious or autoimmune enediated skin disease, abullous skin claease, arthma, allergic rhinitis, atopic dermatitis, psoriasis, an allergic disease, arthma, allergic rhinitis, atopic dermatitis, psoriasis, an allergic confisease, and atransplantation associated disease of the lung, confict disease of the lung, of the invention.

CC of the invention.
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N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosus, rheumatoid arthritis, diabetes mellitus, immune-med renal disease, or demyelinating diseases of the central or periphe
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10-AUG-1993;
27-OCT-1994;
05-JUN-1996;
This invention describes a novel isolated antibody or antibody fragment (I) which selectively binds to a polypeptide encoded by cytokine respor gene 2 (CR2) and modulates CR2 activity. The products of the invention have cytostatic, anti-allergic, immunosuppressive and antimicrobial activity. The antibodies are useful as therapeutic agents for regulating cellular proliferation and differentiation and for treating all kinds of the contraction and differentiation and contractions are useful as the contraction and contraction and contractions are useful as the contraction and contraction
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-Q=/cgn2 1/USPTO_spool_p/US10705757/runat 22092005_115015_22141/app_query.fasta_1.5333
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-DB=PIR -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=blte -START=1 -END=-1 -MATRIX=blosum62 -TRANS=humae40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=200000000
-USER=US10705757 @CGN 1 1256 @runat 22092005 115015_22141 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -WANN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

prot

A;Experimental source: testis
A;Note: testis-specific transcript is shorter and more stable than the somatic transcri.
C;Comment: Pim-1 autophosphorylates at unknown sites. protein kinase (EC 2.7.1.37) pim-1 - rat N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene C;Species: Rattus norvegicus (Norway rat) C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004 R;Wingett, D.; Reeves, R.; Magnuson, N.S.
Nucleic Acids Res. 20, 3183-3189, 1992
Nucleic Acids Res. 20, 3183-3189, 1992
A;Title: Characterization of the testes-specific pim-1 transcript in rat
A;Reference number: S26298; MUID:92319652; PMID:1620615 A;Cross-references: UNIPROT:P26794; EMBL:X63675; NID:g56902; PIDN:CAA45214.1; PID:g5690 A; Molecule type: mRNA A; Residues: 1-313 <WIN> C; Accession: S26298 A; Accession: S26298

C; Function:

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni. A;Note: in testis may be involved in signal transduction events of normal germ cell math C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogen: F;36-290/Domain: protein kinase homology <KIN>F;44-52/Region: protein kinase ATP-binding motif

Percent Similarity:
Best Local Similarity:
Query Match: Score: No . : 5.33e-70 1668.00 100.00% 100.00% 68.28% Length:
Matches:
Conservative:
Mismatches: Gaps: Indels: 313 0 0 0

Lys #status

predicted

US-10-705-757-3 (1-1302) x S26298 (1-313)

4 ATGCTCTTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCAGCCCCTTGCAACGACCTG

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protein kinase (EC 2.7.1.37) pim-1 - human N;Alternate names: kinase-related transforming C;Species: Homo sapiens (man) C;Date: 31-Mar-1989 #sequence revision 07-Oct-1 C;Accession: JU0327; A46554; A27476; I58412
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 07-Oct-1994
C;Accession: JU0327; A46554; Ā27476; I58412
R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.;
Gene 90, 303-307, 1990
A;Title: Primary structure of the putative human or
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A; Cross references: UNIPROT: P11309; GB: M27903; NID: g189958; PIDN: AAA60090.1; PID: g387022

R; Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.

J. Cell: Blochem. 35, 105-112, 1987

A; Title: Cloning and characterization of the human PIM-1 gene: a putative oncogene relat A; Reference number: A46554

A; Accession: A46554

A; Accession: A46554

A; Melecule type: mRNA

A; Residues: 1-313 KEES

A; Fross-references: GB: M24779; NID: g1066790; PIDN: AAA81553.1; PID: g1066791

R; Aakti-Houri, R; Hazum, S; Givol, D; Telerman, A.

Gene 54, 105-111, 1987

A; Flet: The cDNA sequence and gene analysis of the human pim oncogene.

A; A; Residues: A27476; MUID: 87277423; PMID: 3475233

A; Accession: A27476

A; MID: 87277423; PMID: 3475233

A; Accession: A27476

A; MID: 87277423; PMID: 3475233

A; Accession: A27476

A; MID: 87277423; PMID: 3475233

A; Accession: A17476

A; MID: 87277423; PMID: 3475233

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A; MID: 8727423; PMID: 3475
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A;Accession: JU0327
A;Molecule type: DNA
A;Residues: 1-313 <REE>
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; GE
R;Meeker, T.C.; Nagarajan, L.; ar-Rush
J. Cell. Biochem. 35, 105-112, 1987
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Best Local Similarity:
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                                                                                 AACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATTTCCGACTGGGGGGAACTG
                                                                                                                                                                          GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValSerAsp
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TVMSP1

TVMSP1

protein kinase (EC 2.7.1.37) pim-1 - mouse

N;Alternate names: kinase-related transforming protein pim-1; p
C;Species: Mus musculus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_chang;
C;Accession: A24169
R;Selten, G; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.;
Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1;
A;Reference number: A24169; MUID:86272109; PMID:3015420
A;Accession: A24169
A;Molecule type: DNA
A;Residues: 1-313 <SEL>
A;Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Genetics:
A;Gene: pim-1
A;Introns: 28/1; 63/3; 80/3; 203/1; 262/1
C;Superfamily: kinase-related transforming protein; protein kinase-relation; phosphotransferase; protein kinase homology <KUN-
F;36-290/Domain: protein kinase homology <KUN-
F;44-52/Region: protein kinase ATP-binding motif
F;67/Active site: Lys #status predicted
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              ;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoni.;Superfamily: kinase-related transforming protein; protein kinase homology;Keywords: ATP; autophosphorylation;phosphotransferase; proto-oncogene; serine/threon;36-290/Domain: protein kinase homology <KIN>;44-52/Region: protein kinase ATP-binding motif
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Indels:
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843 280 903 240

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protein kinase pim-2 (EC 2.7.1.-) - mouse
C;Species: Mus musculus (house mouse)
C;Pate: 10-Oct-1995 | Heagence revision 21-Jan-1997 | | |
C;Accession: S5533; A43093; B43093
R;Van der Lugt, M.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
R;Van der Lugt, M.M.T.; Domen, J.; Verhoeven, E.; Linders, K.; van der Gulden, H.; Allen
EMBO J. 14, 2536-2544, 1995
A;Flite: Proviral tagging in B-mu-myc transgenic mice lacking the Pim-1 proto-oncogene l
A;Reference number: S55333; MUID:95300786; PMID:7781606
A;Reference sides: 1-370 <VAN
A;Residues: 1-370 <VAN
A;Residues: 1-370 <VAN
A;Residues: Mr., 27-370 <VAN
A;Residues: Mr., 27-370 <VAN
A;Residues: Mr., 27-370 <VAN
A;Residues: Mr., 27-370 <VAN
A;Residues: Mr., 21-370 <V
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                                                    TCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTGGAGAGGCCCGAACCCGT
                                                                                                       uGluValAlaLeuLeuTrpLysValGlyGluGlyAsnGlyHisProGlyValileArgLe
                                                                                                                                                            GGAAGTGGTCCTGCTGAAGAAGGTG-----AGCTCGGGCTTCTCGGGCGTCATTAGACT
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yPheGlyThrValPheAlaGlyHi8ArgValThrAspArgArgGlnValAlaIleLy8Va
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uLeuAspTrpPheGluThrProGluGlyPheMetLeuValLeuGluArgProMetProAl
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A;Reference number: Z19538
A;Recession: T2255
A;Status: preliminary; translated from GB
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; EMBL:
A;Experimental source: Clone F45H7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F45H7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T22Z55
R;Percy, C.
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A;Introns: 72/3; 160/3; 310/1
C;Superfamily: kinase-related transforming protein; protein
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A; Map position: 3
                                         US-10-705-757-3 (1-1302) x T22255 (1-363)
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                                                                                                                                                       Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rPhePheThrGlnValValAlaAlaValGlnHisCysHisAlaArgGlyValValHisAr
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                                                                      7.28e-22
622.50
58.59%
41.10%
25.48%
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                                                                                                            Length:
Matches:
Conservative:
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                                                                                   Mismatches:
Indels:
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134
57
105
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RESULT 6
T15435
hypothetical protein C06E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #to
C;Accession: T15435
R;Favello, A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGCGGCATTGCCACACTGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyGlnGlyLysIleSerGluAspMetAlaArgPheLeuPheArgGlnIleAlaValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGCTGGCCTCCAAC
                                                                                                                                                                                                        pArgSerProProThrSerSerValSerGlnGlnProGlySerAlaAspGluGlyValGl
                                                                                                                                                                                                                                                                                                                                                                               CAGGATGTTCTCCTG------
                                                                                                                                                                                                                                                                                                                                                                                                                 LeuThrPheAspProPheGlnArgCysSerLeuGluAlaIleLeuAsnHisProTrpVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTCCCTGAGACCATCGGACCGGCCCTCCTTTGAAGAAATCCAGAACCATCCGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyProLeuProPhePheValProValSerAlaGluValLysAspLeuIleSerLysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGCCAAGTGTACTTTAGGCAAAGGGTCTCTTCAGAATGTCAACATCTTATTAGATGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerLeuAsnGlyArgLeuProPheArgAsnGluLysAspIleCysThrAlaHisLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValHisGluCysValGlnAsnArgValLeuHisArgAspLeuLysAspGluAsnIleVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysGluTrpAlaArgIle---AsnGlyGluGlnValProMetGluIleCysMetLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCGACTGGGGGAACTGCCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCATCCGCGTCGCCGACAACTTGCCGGTGGCCATCAAGCACGTGGAGAAGGACCGGATT
                                                                                                                                        yLeuSerAlaSerSer
                                                                                                                                                                                                                                            ------CCAGCAAATAGCAGCCATTCTGTCAGACCC---TCCAGGGAAGAGAGAGAGCTTG
                                                                                                                                                                                                                                                                                                              CAGGCCACCGCCGAGATTCATCTGCACAGCCTGTCACCATCAC----
                                                                                                                                                                                                                                                                                                                                               LysGlnGlnThrLeuSerTrpAspAlaLeuThrLysAsnLysValGlnLysLysThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ArgSerGlnTyrSerAspPheGlnGlyThrArgLeuTyrCysProProGluTrpPheLeu
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                                  #text_change 20-Sep-1999
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Best Local Similarity:
Query Match:
DB:
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A;Molecule type: DNA
A;Residues: 1-409 <FAV>
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A;Experimental source: strain Bristol N2
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                 GATATTCCATTTGAGCACGACGAAGAGATCGTCAAGGGCCAAGTGTACTTTAGGCAAAGG
                                                   LeuProLeuGluAlaThrSerTrpSerLeuGlyValLeuLeuPheIleLeuLeuThrGly
                                                                                                                    {\tt LysGluPheGlnGlyThrArgSerTyrCysProProGluTrpPheArgAspGlnLeuTyr}
                                                                                                                                                        ACGGACTTTGACGGAACCCCGAGTGTACAGTCCTCCAGAGTGGATTCGCTACCATCGCTAC
                                                                                                                                                                                        ||||||:::||||||:::|||||||||::: |||
ThrGlyGluValLysLeuValAspPheGlyAlaThrAlaTyrAlaGluLysAlaThrLys
                                                                                                                                                                                                          CGCGGCGAACTCAAACTCATCGACTTCGGGGTCGGGGGGCGCTGCTCAAGGACACAGTCTAC
                                                                                                                                                                                                                                                            SerLysHisGlyLeuLeuHisArgAspIleLysAspGluAsnLeuIleValAsnMetAsn
                                                                                                                                                                                                                                                                                AAC---TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAAC
                                                                                                                                                                                                                                                                                                                             AsnGluAspMetGlyLysPheIlePheLysGlnValIleThrThrValPheAsnMetTyr
                                                                                                                                                                                                                                                                                                                                                                                             MetGluArgProAlaAsnCysMetAspLeuPheAspMetValSerValHisGlyProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetThrCysArgGlnLeuIleProSerGluValCysHisLeu---GluThrCysGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGCCCAACGGCACCCGAGTGCCCATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGC
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GlyGlnGlnProValAlaValLysPheValGlnHisLysHisValArgSerTrp---Thr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTTCGGCTTACTCGGGCATCCGCGTCGCCGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MetIleLysArgLysLeuGlnAspLeuAlaValCysCysSerTyrGlnValAspPheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAspGluIleGlyArgGlyGlyPheGlyIleValTyrGluAlaThrThrArgGlnAsp
                                                                                    CACGGCAGGTCGGCTGCTGTTTGGTCCCTGGGGATCCTGCTCTATGACATGGTCTGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76/3;
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Matches:
Conservative:
Mismatches:
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360 94 300

240

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probable serine/threonine-specific protein kinase ();Alternate names: SNF1-related protein kinase ()Species: Cucumis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T10449 R;Gumpel, N.J.
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Query Match:
DB:
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A;Experimental source: cv. Masterpiece; cotyledon
C;Function:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-serine-phosphate 
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A;Title: Structure and expression of a gene from Arabidopsis A;Reference number: JC1446; MUID:93013041; PMID:1339373 A;Accession: JC1446 A;Molecule type: DNA A;Residues: 1-512 <-LEG A;Residues: 1-512 <-LEG A;Trons-references: UNLTGROT:038997; GB:M93023; NID:g166599; R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
                                                                                                                                                                 serine/threonine-specific protein kinase (EC 2.7.1. N;Alternate names: protein kinase SNF1 homology C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 C;Accession: JC1446; SS8266; S66334 R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.C Gene 120, 249-254, 1992
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PID:g166600
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A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3 C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or pepticyserfamily: AMP-activated protein kinase; protein kinase homology C;Kuywordds: ATP, magnesium; phosphotransferase; serine/threonine-specific; P;17-271/Domain: protein kinase homology cKINs P;25-33/Region: protein kinase ATP-binding motif F;140,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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A,Description: Dil
A,Reference number
A,Accession: S5826
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A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: EMBL:X86966;
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A;Residues: 144-198 <THU>
A;Crose-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1;
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Dittrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 nov
A;Reference number: S66314; MUID:96123233; PMID:8534852
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 CTGCTCAAGGACACAGTCTACACGGACTTTGAC---:::::::::|||
                                                                                         AACATCTTAATCGACCTGAACCGCGGCGAACTCAAACTCATCGACTTCGGGTCGGGGGCG
                                                                                                                                                                                                      TyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgAsnPhePheGlnGlnIle
                                                                                                                                                                                                                                         TTCATCACCGAGCGAGGAGCCCTCCAGGAGGAGCTGGCCGGAGCTTCTTCTGGCAGGTG
                                                                                                                                                                                                                                                                                  ThrProThrAspIleTyrLeuValMetGluTyrValAsnSer---GlyGluLeuPheAsp
                                                                                                                                                                                                                                                                                                                       AGGCCCGATAGTTTCGTGCTGATCCTGGAGAGGCCCGAACCCGTGCAAGACCTCTTCGAC
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                                                        AsnLeuLeuLeuAsp---SerLysCysAsnValLysIleAlaAspPheGlyLeuSerAsn
                                                                                                                                IleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAspLeuLysProGlu
                                                                                                                                                                     CTGGAGGCCGTGCGGCATTGCCACAACTGCGGGGTTCTCCACCGCGACATCAAGGACGAG
                                                                                                                                                                                                                                                                                                                                                            IleLeuArgLeuPheMet-----HisProHisIleIleArgLeuTyrGluValIleGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgLysIleLysAsn-----MetGluMetGluGluLysValArgArgGluIleLys
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Differential accumulation of the transcripts of 22
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T13741
T13741
hypothetical protein 2285.8 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 0
C;Accession: T13741
R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of Drosophila m
   Query Match:
DB:
                                      Percent Similarity:
Best Local Similarity:
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A; Residues: 1-1398 < MUR>
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29.17%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Mech. Dev. 48, 153-164, 1994

A;Title: Identification of novel protein kinases expressed in the first of the first o
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C;Species: Mus musculus (house mouse)
C;Date: 02-7ull-1996 #sequence revision 02-Jul-1996 #text_change 16-Aug-2004
C;Accession: I49072
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    CAAGACCTCTTCGACTTCATCACCGAGCGAGGAGCCCTCCAGGAGGAGCTGGCCCGGAGC
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N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 16-Aug-2004
C;Accession: S66730
R;Ansorge, W.; Benes, V.; Rechmann, S.; Schwager, C.; Teodoru, C.; Voss, H.; Wiems submitted to the Protein Sequence Database, July 1996
A;Reference number: S66723
A;Accession: S66730
A;Molecule type: DNA
A;Residues: 1-1101 <ANS
A;Cross-references: UNIPROT:Q08217; EMBL:Z74788; NID:g1419846; PIDN:CAA99051.1; PJ
A;Cross-references: SGD:S0005405
A;Cross-references: SGD:S0005405
A;Map position: 15L
C;Superfamily: protein kinase homology
C;Keywords: ATP
F;839-1099/Domain: protein kinase homology <KIN>
F;847-855/Region: protein kinase homology <KIN>
F;847-855/Region: protein kinase ATP-binding motif
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                                                   SerAspPheThrIleLeuGlnValMetGlyGluGlyAlaTyrGlyLysValAsnLeuCys
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GlyGluMetPheAspTyrLeuThrSerAsnGlyHisLeuSerGluAsnGluAlaArgGln
                                                                                        TCGCAGTACCAGGTGGGCCGCTGTTTGGGCAGCGGTGGCTTCGGCTCGGTCTACTCGGGC
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Conservative:
Mismatches:
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A;Gene: AKIN11
C;Function:
C;Function:
EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, complements SNF1 mutations in yeast
                                                                                        A;Cross-references: UNIPROT:P92958; EMBL:X99279; A;Experimental source: cultivar Columbia C;Genetics:
                                                                                                                                                  C;Accession: T52633

R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis A;Reference number: Z25116; MUID:99238528; PMID:10220464

A;Accession: T52633

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
A;Residues: 1-512 <BHA>
                                                                                                                                                                                                                                                                                                                                       serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis N;Alternate names: SNF1 protein kinase omolog AKIN11 [validated] - Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 09-Jul-2004
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> protein Machi <u>Z</u>

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;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
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LeuProArgTyrLeuAlaValSerProPro--
                                     crg---cacagocrgroacoarcacoagoaaaragoagocatrotgroagaccorocag
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A;Accession: A56009
A;Accession: A56009
A;Accession: A56009
A;Accession: A56009
A;Accession: A56009
A;Accession: A56009
A;Cross-references: UNIPROT:Q40544; GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
A;Cross-references: UNIPROT:Q40544; GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonir
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-3J/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C;Accession: A56009
R;Muranaka, T; Banno, H; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
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  GACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTGGAGAGGCCCCGAACCCCGTGCAA
                                                                                   ATGGAAGTGGTCCTGCTGAAGAAGGTGAGCTCGGGCCTTCTCGGGCCGTCATTAGACTTCTG
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Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 14
T20941
T20941
hypothetical protein F15A2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text.
C;Accession: T20941
R;Gregory, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19349
A;Accession: T20941
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-887 <WIL>
A;Cross-references: UNIFROT:019469; EMBL:Z70207; PIDN:CAJ
A;Cross-references: UNIFROT:019469; EMBL:Z70207; PIDN:CAJ
A;Gene: CESP;F15A2.6
A;Map position: X
A;Introns: 32/1; 63/3; 92/2; 139/2; 189/3; 328/2; 448/2;
Alignment Scores:
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Score:
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Length:
Matches:
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LeuLeuLeuGluHisValSerGly---GlyGluLeuPheAspTyrLeuValArgLysGly
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                                            SerIleAspProAspValLeuArgHisMetAsnCysLeuGlyCysPheLysAspLys-Gl
                                                                          AGCTTGTCTGCTGGC----CTCCAACAGGACCCTGCTCTACGATGC---AGGGACAGAAAT
                                                                                                                                                                        SerGlyThr-----ThrLysAlaAspProGluLeuGluLeu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCTACACGGACTTTGACGGAACCCGAGTGTACAGTCCTCCAGAGTGGATTCGCTACCAT
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probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YAL002; protein YAL017w; secretory protein SSP138
C;Species: Saccharomyces cerevisiae
C;Date: 30-659-1993 #sequence revision 02-Aug-1994 #text_change 16-Aug-2004
C;Accession: S33653; S36717; S36732; JH0486
R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B.F.F.; Barton, A.; Kabac
Yeast 9, 543-549, 1993
A;Title: The YAL017 gene on the left arm of chromosome I of Saccharomyces cerevisiae end
A;Reference number: S33653; MUID:3311122; PMID:8322517
A;Accession: S33653
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; I
Submitted to the EMBL Data Library, January 1993
A;Reference number: S36711
A;Accession: S36717
A;Accession: S36717
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Zhong, W.; Zeng, B.; Fortin, N.; I
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
A;Malecule type: DNA
A;Reference number: S22266; MUID:9221690; PMID:1561836
A;Accession: S3672
A;Accession: S3673
A;Accession: S3673
Gene 107, 111-118, 1991

A; Title: Selection of secretory protein-encoding genes by fusion with PHO5 in Sac A; Reference number: JHO483; MUID:92077420; PMID:1743509

A; Acetesion: JHO486

A; Molecule type: DNA

A; Residues: 1-72,'E',74-154 <SID>
C; Genetics:

A; Gene: SCD:FUN31; SSP138

A; Cross-references: SGD:S0000015; MIPS:YAL017w

A; Cross-references: SGD:S0000015; MIPS:YAL017w

C; Superfamily: protein kinase homology
C; Superfamily: protein kinase homology <KIN>
F; 1104-1112/Region: protein kinase homology <KIN>
F; 1104-1112/Region: protein kinase homology <KIN>
F; 1104-1112/Region: protein kinase homology over the content of the content 
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ene 107, 111-118, 1991
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Sidhu, R.S.; Mathewes, S.; Bollon,
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R.K.; Barton, A.; Kaback, D.B.; Bussey, H.
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                                                                                      TTTAGG-----CAAAGGGTCTCTTCAGAATGTCAACATCTTATTAGATGGTGCCTGTCC
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Result
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-MoDEXT=0 - UNITS-Site -STRATE-1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LOCEXT=0 -UNITS-Site -STRATE-1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODEL-COCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10705757 @CGN 1 1_137 @run +HEAPSIZE=500 -MINLEN=0 -NCBU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
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ALIGNMENTS

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US-09-237-543-7
Sequence 7, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
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Best Local Similarity:
                                                                                                                          US-10-705-757-5 (1-942) x US-09-237-543-7 (1-313)
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LENGTH: 313
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US-09-644-450-7

Sequence 7, Application US/09644450

Patent No. 6383791

GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: MOVEL MOLECULES OF THE
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
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Sequence 8, Application US/09237543A

Patent No. 6143540

GENERAL INFORMATION:

APPLICANT: Kapeller, Rosana

TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: 035800/175631

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT APPLICATION NUMBER: US/09/237,543A

CURRENT FILING DATE: 1999-01-26

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 8

LENGTH: 313

TYPE: PRT

ORGANISM: Rattus norvegicus
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DB:
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SEQ ID NO 8
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TYPE: PRT
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APPLICANT: KAPELICAN, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF TH
TITLE OF INVENTION: AND USES THEREOP
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
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Mismatches:
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Sequence 9, Application US/09237543A
Patent No. 6143540
GENERAL INFORMATION:
APPLICANT: KAPELIER, ROBANA
TITLE OF INVENTION: NOVEL MOLECULES OF T
FILE REFERENCE: 035800/175631
CURRENT APPLICATION NUMBER: US/09/237,54
CURRENT FILLING DATE: 199-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9
SEQ ID NO 9
SEQ ID NO 9
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-237-543-9
                Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                     Alignment Scores:
Pred. No.:
Score:
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      (1-942)
                 3.57e-136
1582.00
97.12%
93.93%
90.45%
      x US-09-237-543-9 (1-313)
                Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 9, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
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            PROTEIN FAMILY
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CURRENT APPLICATION NUMBER: US/09/644,450
CURRENT FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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TCAGAGTGTCAGCACCTTATTAAATGGTGCCTGTCCCTGAGACCGTCAGATCGGCCCTCC
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Mismatches:
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Sequence 26, Application US/08463081B

; Sequence 26, Application US/08463081B

; Patent No. 5871960
; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION: Mucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and EX
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/463,081
FILLING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/104,731
FILLING DATE: 10-AUG-193
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/796,06
FILLING DATE: 20-NOV-91
APPLICATION UNMBER: US 07/796,06
FILLING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: VIviana Amzel, Ph. D.
REGISTRATION UNMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38
TELECOMMUNICATION INFORMATION:
TELEPAX: (213) 622-7700
TELEPAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TELEPAX: n.a.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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Conservative:
Mismatches:
Indels:
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RESULT 8
US-08-461-379A-26
; Sequence 26, Application US/08461379A
; Patent No. 5871961
; Patent No. 5871961
; Patent No. 1871961
; GENERAL INFORMATION: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
ADDRESSEE: . (B) STREET:One Westlakes-Berwyn
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STATE: Pennsylvania
COUNTRY: USA:
ZIP: 19482

ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NUMBER: US/08/96,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
APPORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELEPHONE: (610)470-0710
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDUSS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
US-08-461-379A-26
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Best Local Similarity:
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                               GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
                                          GAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCCTACAG
                                                                    TCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTG
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1580.00
97.12%
93.93%
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Matches:
Conservative:
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Indels:
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RESULT 9
US-08-462-390B-26
# Sequence 26, App
# Patent No. 58828
APPLICATION NUMBER: US/08/462,390B FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
REFERENCE/DOCKET NUMBER: TELEPHONE: (610)407-0700
TELEPAX: (610)407-0700
TELEPAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 26;
                                                                                                                                                                                                                                                                                                                        Sequence 26, Application Patent No. 5882894 GENERAL INFORMATION:
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM COMPUTER: COMPUTER: PALENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, V
TITLE OF INVENTION: Transformed Cell Thereof, and Expression
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
                                                                                                                                                                                                                   ADDRESSEE:
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
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LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 10
US-08-463-074B-26
; Sequence 26, App
; Patent No. 60201
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                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
RELECOMONICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEPHONE: (213) 622-7700
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                    US-08-463-074B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: US 08/104,736
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Smith, Kendall A. & Beadling, Carol TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               TOPOLOGY: n
MOLECULE TYPE:
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                                                                                                                                                                                                 No.:
                                                                                                                                                 Match:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                       TYPE: peptide
STRANDEDNESS: n.a.
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Matches:
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US-08-465-585C-26
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                                                                                            Sequence 26, Application US/08465585C

Patent No. 6027914,
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
                                                      NUMBER OF COURSES
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
(B) STREET:
COMPUTER READABLE FORM:
          ADDRESSEE:
CITY: Los Angeles
STATE: Californiaa
COUNTRY: USA
ZIP: 900071
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APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995

PRIOR APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: V1v1ana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: 966 38149 (DART-050)
TELECOMMUNICATION: TROPRMATION:
TELEPAX: (213) 622-7700
TELEPAX: (213) 622-7700
TELEPAX: (213) 632-7700
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TELEPAX: (313) 632-7700
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Best Local Similarity:
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TOPOLOGY: n.a.
MOLECULE TYPE: pepti
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAGCCGCGGC
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93.93%
90.34%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Sequence 26, Applicate
Sequence 26, Applicate
Sequence 26, Applicate
Patent No. 6057427
Patent No. 6057427
Patent No. 6057427
PATENTION: Mucleic Acids Encoding CR5
TITLE OF INVENTION: Polypeptide, Vector and Transformed
TITLE OF INVENTION: Expression Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-08-652-446-26
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                                                        APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRICH APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRICH APPLICATION DATA:
                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nuc.
TITLE OF INVENTION: Poly
TITLE OF INVENTION: Expi
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCI
ADDRESSEE: LOB Angeles
STATE: California
             APPLICATION NUMBER: 08/462,337 FILING DATE: 5-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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(B) STREET:
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PRIOR APPLICATION DATA:

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Best Local Similarity:
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FILING DATE: 5-JUN-1995
PRIOR APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION NUMBER: 08/739,523
PRIOR APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-196
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
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                                                GAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC
                                                                                                   GluArgÞroGluÞroValGlnAspLeuPheAspÞheIleThrGluArgGlyAlaLeuGln
                                                                                                                              GAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCTACAG
                                                                                                                                                                      SerGlyVallleArgLeuLeuAspTrpPheGluArgProAspSerPheValLeuIleLeu
                                                                                                                                                                                                                                                                   CCCAATGGCACCCGAGTGCCCATGGAAGTGGTCCTGTTGAAGAAGGTGAGCTCGGACTTC
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90.34%
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Matches:
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Mismatches:
Indels:
Gaps:
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RESULT 13
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APPLICANT: Benner
                                                                                                                      TELEX: none
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: amino acid
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 03/25/92
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                   ZIP: (note: this is an international post code)
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Benner, Steven A.
TITLE OF INVENTION: Predicting Folded Structures of Proteins
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven A. Benner
STREET: Hadlaubstrasse 151
                                   ORGANISM: rat FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                               TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                               PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION: (International)
                                                                      ORIGINAL SOURCE:
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CITY: Z
STATE:
AUTHORS:
AUTHORS:
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                                                                                   DESCRIPTION:
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RESULT 14
US-09-237-543-5
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Best Local Similarity:
Query Match:
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TITLE: The protein kinase f:
; JOURNAL: Science
VOLUME: 241
; PAGES: 42-52
; DATE: 1988
US-07-857-224B-41
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                                                                                                                                                                                                                                         Application US/09237543A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Patent No. 6143540
; GENERAL INFORMATION:
APPLICANT: KAPELLER, ROSANA
TITLE OF INVENTION: NOVEL MOLECULES OF 1
; TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 035800/175631
; CURRENT APPLICATION NUMBER: US/09/237,54
; CURRENT FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity:
Query Match:
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ATCTTAATCGACCTGAGCCGCGGCGAAATCAAACTCATCGACTTCGGGTCGGGGGGCGCTG
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ThrGluTrpGlySerLeu---GlyGlyMetAlaValProLeuGluValValLeuLeuArg
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81.33%
71.00%
64.18%
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162 162 185 222 205 282

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Sequence 5, Application US/09644450

Patent No. 6383791

GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
ITILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
ITILE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
CURRENT APPLICATION NUMBER: US/09/644,450

CURRENT FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 455
CORGANISM: Rattus norvegicus
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Search completed: September 22, 2005, 17:24:43 Job time: 32.7742 secs

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-MOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
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ALIGNMENTS

RESULT 1 ABG33015 HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disordacute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; WM; mouse. 26-JAN-1999; 99US-00237543; 23-AUG-2000; 2000US-00644450. 04-OCT-2001; 2001US-00971791. US2002115120-A1. ABG33015 standard; Kapeller-Libermann R, 22-AUG-2002. Mus musculus. Mouse protein kinase phosphorylation site. 20-DEC-2002 (first entry) ABG33015; (MILL-) MILLENNIUM PHARM INC 2002-712471/77. protein; Rudolph-Owen LA, 313 ₽ Macbeth 7. disorder; emia; CML;

pro

Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                  Alignment
                                                                                                                                                                                                                                                                                             The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIM1 or PIM3 kinase. PIM1 and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for identifying analgesics, chronic pain, by screening compound kinase, or related compounds.
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Mouse; PIM-1; protein kinase; enzyme serine/threonine protein kinase PIM-1.

2003WO-EP000492

19-JAN-2002; 2002EP-00001401

AVENTIS PHARMA DEUT GMBH

Mueller G, Schneider ₩, Techank

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New human or murine PIM-3 DNAs or polypeptides, useful for as agent for identifying anti-type 2 diabetes mellitus drugs, or treating insulin resistance or type 2 diabetes mellitus. a screening

Page 40; 40pp; English.

The present sequence is the protein sequence of the murine serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 prote are the paralogues of novel human and murine PIM-3 proteins (see ABR62 and ABR6293)) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved the development of insulin resistance and type 2 diabetes mellitus. Th invention relates to the use of PIM-3 nucleic acids and proteins in: screening assays for compounds that modulate insulin resistance or type diabetes mellitus; detection assays for detecting insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, forensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type diabetes mellitus proteins
ABR62932 type The ä N

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Percent Similarity:
Best Local Similarity:
Query Match: 5.03e-139 1668.00 100.00% 100.00% 95.37% Conservative: Mismatches: Indels: Gaps: 313 0 0 0

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Db	1 MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaArgProCysAsnAspLeu 20	
8	61 CACGCCACCAAGCTGGCCCGGGCAAAGAAGAAGGAGCCCCTGGAGTCGCAGTACCAGGTG 120	J
DЬ	21 HisAlaThrLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal 40	
Ş	121 GGCCGGCTGTTGGGCAGCGGTGGCTTCGGCTCTACTCTGGCATCCGCGGTCGCCGAC 180	J
90	41 GlyProLeuLeuGlySerGlyGlyPheGlySerValTyrSerGlyIleArgValAlaAsp 60	
Ś	181 AACTTGCCGGTGGCCATTAAGCACGTGGAGAAGGACCGGATTTCCGATTGGGGAGAACTG 240	Ü
90	61 ABNLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu 80	
ð	241 CCCAATGGCACCCGAGTGCCCATGGAAGTGGTCCTGTTGAAGAAGGTGAGCTCGGACTTC 300	•
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CC identification of the mediators is useful since they are potential CC therapeutic targets. The present sequence represents murine Piml.
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                                                 GAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCTACAG
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16-SEP-2002; 2
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02-JAN-2003; 2
The present invention relates to a method of designing a ligand binding to a target molecule. The method involves identifying as molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesising ligand. The invention is useful for designing drug products and for designing ligand binding to target molecules such as nuclear hormone receptors, TNF receptors, G-protein coupled receptors, methyl transferases, ligases, etc. The present sequence is the Mus musculus PIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular
G-protein
                                                                                                                                                                   Designing a ligand binding to a target molecule, comprises identifying molecular scaffolds compounds binding to members of a molecular family, detecting orientation of scaffolds at a binding site of target, and synthesizing ligand.
                                                                                                                                           Disclosure;
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coupled receptor;
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2002US-0411398P.
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                                                                               TCAGAGTGTCAGCACCTTATTAAATGGTGCCTGTCCCTGAGACCGTCAGATCGGCCCTCC
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                                                                                                        US-10-705-757-5
                                                                                                                                                                                                                                                                                                                                                                            The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method i useful for modulating the level or activity of HKID-1 polypeptide or polymucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous leukaemia (CMI) and Waldenstrom's macroglobulinaemia (MM). This is the action acid accurace of a rat protein kinase phemorylation acids accurace.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HKID-1; serine/threonine kinase; cellular proliferative disorder; differentiative disorder; cancer; haematopoietic neoplastic disorder; Acute promyeloid leukaemia; APML; Chronic myelogenous leukaemia; CML; Waldenstrom's macroglobulinaemia; WM; rat.
                                                                                                                                                                                                                                                                                                                      Sequence
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for identifying analgesics, useful particularly for treating c pain, by screening compounds for interaction with PIM-1 or
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or related compounds.
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                                                                                                                                                                                                                                                                                                                               CACGCCACCAAGCTGGCGCCGGGCAAAGAGAAGGAGCCCCTTGGAGTCGCAGTACCAGGTG
                                                                                                                                                                                                                                                                                                                                                                      ATGCTCCTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCCCCGCCCCCTGCAACGACCTG
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                                                               GAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCTACAG
                                                                                                               TCGGGCGTCATTAGACTTCTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTG
                                                                                                                                                                CCCAATGGCACCCGAGTGCCCATGGAAGTGGTCCTGTTGAAGAAGGTGAGCTCGGACTTC
                                                                                                                                                                                                    AsnLeuProValAlaIleLysHisValGluLysAspArgIleSerAspTrpGlyGluLeu
                                                                                                                                                                                                                                                                             GCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCTACTCTGGCATCCGCGTCGCCGAC
                                                                                                                                                                                                                                                                                                        HisAlaAsnLysLeuAlaProGlyLysGluLysGluProLeuGluSerGlnTyrGlnVal
                                                                                                                                                                                                                                                                                                                                                      MetLeuLeuSerLysIleAsnSerLeuAlaHisLeuArgAlaAlaProCysAsnAspLeu
GluGluLeuAlaArgSerPhePheTrpGlnValLeuGluAlaValArgHisCysHisAsn
                                                                                                                                                   ProAsnGlyThrArgValProMetGluValValLeuLeuLysLysValSerSerGlyPhe
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agent for treating

for

Example 2; Page 39; 40pp;

English.

The present sequence is the protein sequence of the rat serine/threonine protein kinase and proto-oncogene, PIM-1. PIM-1 proteins are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 and ABR62933) of the invention, which are therefore expected to be involved in cancer and cell growth regulation. PIM-3 is also involved in the development of insulin resistance and type 2 diabetes mellitus. The invention relates to the use of PIM-3 nucleic acids and proteins in:

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RESULT 8
ABR62338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVENTIS
                                                                                                                                                                                                                                             n or murine PIM-3 DNAs or polypeptides, useful for ridentifying anti-type 2 diabetes mellitus drugs, insulin resistance or type 2 diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                            Mueller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              screening assays for compounds that modulate insulin resistance or type diabetes mellitus; detection assays for detecting insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, forensic biology); predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, pharmacogenomics); and for the preparing a medicament for the treatment of insulin resistance or type idabetes mellitus
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                                          CCGTTTGAGCACGATGAAGAGATCATCAAGGGCCAAGTGTTCTTCAGGCAAACTGTCTCT
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                                                                                                                                                                            The present sequence is the protein sequence of human Piml, a protein related to tyrosine threonine kinase (TTK, see ABP54938). TTK polynucleotides and polypeptides of the invention encompass polynucleotides and polypeptides having sequence similarity or sequence identity to human TTK and other genes and gene products related to TTK, such as Piml. The invention is based on the finding that TTK is differentially expressed in various forms of cancer. It provides methods for the identification of cancerous cells, especially breast cancer and colon cancer cells, by detection of expression levels of TTK, as well as diagnostic, prognostic and therapy. Assays for identifying molecules that modulate the activity of these genes in cancers, as well as methods of inhibiting tumour growth by inhibiting the activity of TTK are also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reducing growth of cancer cells comprises reducing Tyrosine Threonine Kinase (TTK) activity, useful in diagnosing and treating disorders with abnormal expression levels and activity of TTK, such as lung, colon,
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N-PSDB; ABV73989.
                                                                                           Sequence 313
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mitotic checkpoint; colon cancer; breast cancer; tumour; cytostatic;
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23-AUG-2000;
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The invention describes a method of modulating the level or activity of human HKID-1 polypeptide, a member of serine/threonine kinase superfamily. The method involves contacting a cell expressing the polypeptide or nucleic acid with an agent to modulate the level or activity of polypeptide, or level of nucleic acid molecule. The method is useful for modulating the level or activity of HKID-1 polypeptide or polymucleotide in a subject having or predisposed to having a disorder involving cancer. Modulating HKID-1 expression or activity is useful for therapeutic purposes, for treating cellular proliferative and/or differentiative disorders including cancer or haematopoietic neoplastic disorders e.g. Acute promyeloid leukaemia (APML), Chronic myelogenous leukaemia (APML) and Waldenstrom's macroglobulinaemia (WM). This is the Modulating levels or activity of HKID-1 polypeptides, a member of serine/threonine kinase superfamily, for treating cancer, by contacting cell expressing the polypeptide with a modulator of the polypeptide. Example Page 40-41; 48pp; English.

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sequence of a human

protein kinase

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kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method of identifying pain-regulating compounds, involving screening candidate compounds for interaction with PIMI or PIM3 kinase. PIMI and PIM3 proteins and coding sequences are useful for treating chronic pain, particularly of neuropathic or inflammatory origin (e.g. where associated with diabetes, cancer, AIDS or neurodegenerative diseases). The present sequence is human PIMI kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 313
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                                                                                                                                                                                                                                                                                                      GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCTGGTCTCTGGCATCCGCGTCGCCGAC
                                                                                                                                                                                                                                                                                                                                           CACGCCACCAAGCTGGCGCCGGGCAAAGAGAAGGAGGCCCCTGGAGTCGCAGTACCAGGTG
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GluArgProGluProValGlnAspLeuPheAspPheIleThrGluArgGlyAlaLeuGln
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The invention relates to detecting cancer (other than ovarian cancer) in a subject, comprising comparing the expression levels of tyrosine threonine kinase (TTK, a mitotic checkpoint gene) polypeptide or polymucleotide in a test cell obtained from the subject and in a normal non-cancer cell, where an increase in the expression level of TTK protein or nucleic acid in the test cell compared to that in the normal cell, indicates the presence of cancer other than ovarian cancer. Also included are reducing growth of a cancerous cell (by contacting a cancerous cell with an amount of an agent effective to reduce TTK polypeptide activity in the cell), an assay for identifying a candidate agent that reduces growth of a cancerous cell (comparising: (1) detecting the activity of a TTK polypeptide in the presence of a candidate agent; and (ii) comparing the activity of TTK polypeptide in the presence of a candidate agent
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 34-35;
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(JEFF/) JEFFERSON A B.
(CHAN/) CHAN V W.
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cc serine/threonine protein kinase and proto-oncogene, PIM-1 Proteins cc are the paralogues of novel human and murine PIM-3 proteins (see ABR62932 cc and ABR62933) of the invention, which are therefore expected to be crimvolved in cancer and cell growth regulation. PIM-3 is also involved in che development of insulin resistance and type 2 diabetes mellitus. The cc invention relates to the use of PIM-3 nucleic acids and proteins in: cc screening assays for compounds that modulate insulin resistance or type 2 diabetes mellitus, detection assays for detecting insulin resistance or type 2 diabetes mellitus (e.g. chromosomal mapping, tissue typing, cc forensic biology); predictive medicine (e.g. diagnostic or prognostic cassays, monitoring clinical trials, pharmacogenomics); and for the cc preparing a medicament for the treatment of insulin resistance or type 2 diabetes mellitus
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CC claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence cc which is differentially regulated in an animal subjected to pain and a cc kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence cc that is differentially expressed in neuronal tissue of a first animal cc subjected to pain, a method for identifying an agent compound that regulates the activity of one or more of the expression of a polynucleotide sequence which is differentially cc expressed in an animal subjected to pain, a method for identifying a compound which regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a compound that regulates the activity in an animal of one or more of the polynucleotides, a method for identifying a compound useful in treating cc pain and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polynucleotide or the compound that cc polypeptides or their antibodies. The polynucleotide or the compound that composition comprising a medicament for treating compain (e.g. spinal segmental nerve injury (Chung), chronic constriction confur confur construction which is a differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed confusion, but was obtained in electronic form directly from WIPO at confusion to the confusion of the printed confusion of the printed
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GENBANK; AAA60089.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -NODEL-STAME+ N2D..model - DEV=xlp
-NODEL-STAME+ N2D..model - DEV=xlp
-O-/cgn2_1/USETO_spool_p/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-O-/cgn2_1/USETO_spool_p/US10705757/runat_22092005_115015_22141/app_query.fasta_1.5333
-DB=PIR -QFMT=fastan - SUFPIX=n2p_rpr -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=blts -START=1 - END=-1 -MATRIX=blosum62 - TRANS=human140.cd1 - LISET=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10705757 @GCN 1 _256 @runat_22092005_115015_22141 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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ore greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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2: pir2:
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Ygapop 10.0 , Ygapext
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ALIGNMENTS

protein kinase (EC 2.7.1.37) pim-1 - mouse
N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene
C;Species: Mus muscullus (house mouse)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A24169 C;Superfamily: kinase-related transforming protein; protein kinase homolog C;Keywords: ATP; autophosphorylation; phosphotransferase; proto-oncogene; F;36-290/Domain: protein kinase homology <KIN>F;44-52/Region: protein kinase ATP-binding motif R;Selten, G.; Cuypers, H.T.; Boelens, W.; Robanus-Maandag, E.; Verbeek, J.; Domen, J.; Cell 46, 603-611, 1986
A;Title: The primary structure of the putative oncogene pim-1 shows extensive homology A;Reference number: A24169; MUID:86272109; PMID:3015420 Best Local Similarity: Query Match: A;Cross-references: UNIPROT:P06803; GB:M13945; GB:M13946; NID:g200352; PIDN:AAA39930.1; C;Comment: Pim-1 autophosphorylates at unknown sites. A; Molecule type: DNA A; Residues: 1-313 < SEL> score: Alignment Scores: F;67/Active site: Lys #status A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonic C; Function: A; Introns: 28/1; 63/3; 80/3; 203/1; 262/1 A;Gene: pim-1 C; Genetics: A; Accession: A24169 Percent Similarity: No.: 4.93e-72 1668.00 100.00% 100.00% 95.37% predicted Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 313 313 0 serine/threon prot

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1 ATGCTCCTGTCCAAGATCAACTCCCTGGCCCACCTGCGCGCCCCGCCCCTGCAACGACCTG

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RESULT 2
$26298

protein kinase (EC 2.7.1.37) pim-1 - rat
N;Alternate names: kinase-related transforming prote
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1994 #sequence_revision 21-Jan-1997;
C;Date: 25-Feb-1994 #
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A;Reference number: S26298; MUID:92319652; PMID:1620615
A;Accession: S26298
A;Molecule type: mRNA
A;Residues: 1-313 <WIN>
A;Residues: 1-313 <WIN>
A;Cross-references: UNIPROT:P26794; EMBL:X63675; NID:g56902; PIDN:CAA45214.1; PID:g56903
A;Cross-references: UNIPROT:P26794; EMBL:X63675; NID:g56902; PIDN:CAA45214.1; PID:g56903
A;Experimental source: testis
A;Bxperimental source: transcript is shorter and more stable than the somatic transcript cycomment: Pim-1 autophosphorylates at unknown sites.
C;Comment: Pim-1 autophosphorylates at unknown sites.
C;Function:
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin A;Note: in testis may be involved in signal transduction events of normal germ cell matu C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;36-290/Domain: protein kinase homology <KIN>F;44-52/Region: protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
                                                                                                                                                           GGCCCGCTGTTGGGCAGCGGTGGCTTCGGCTCCGGTCTACTCTGGCATCCCGGTCGCCGAC
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GluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuLysAspThrValTyrThrAsp
                                                                                                      GAAATCAAACTCATCGACTTCGGGTCGGGGGCGCTGCTCAAGGACACAGTCTACACGGAC
                                                                                                                                                                                                                                            GAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAAC
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A;Mclecule type: DNA
A;Residues: 1-313 <REE>
A;Cross-references: UNIPROT:P11309; GB:M27903; NID:g189958; PIDN:AAA6
A;Cross-references: UNIPROT:P11309; GB:M27903; NID:g189958; PIDN:AAA6
R;Meeker, T.C.; Nagarajan, L.; ar-Rushdi, A.; Croce, C.M.
J. Cell. Biochem. 35, 105-112, 1987
A;Title: Cloning and characterization of the human PIM-1 gene: a puts
A;Reference number: A46554; MUID:88115604; PMID:3429489
A;Reference number: A46554
A;Residues: 1-313 <MEE>
A;Cross-references: GB:M24779; NID:g1066790; PIDN:AAA81553.1; PID:g10
R;Zakut-Houri, R.; Hazum, S.; Givol, D.; Telerman, A.
Gene 54, 105-111, 1987
                                 A;Cross-references: GB:M54915; NID:g189961; PIDN:AAA36447.1; PID C;Comment: Pim-1 autophosphorylates at unknown sites. C;Genetics:
A;Gene: GDB:PIM1
A;Cross-references: GDB:119495; OMIM:164960
A;Map position: 6p21.2-6p21.2
A;Introns: 28/2; 63/3; 80/3; 203/1; 262/1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosph C;Superfamily: kinase-related transforming protein; protein kinas C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinas C;Keywords: ATP; autophosphorylation; phosphoprotein; protein kinase ATP-binding motif F;67/Active site: Lys #status predicted
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A; Residues: 1-14, 'RA', 17-313 < ZAK'>
A; Cross references: GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:g189957
A; Cross references: GB:M16750; NID:g189956; PIDN:AAA60089.1; PID:g189957
R; Domen, J: Von Lindern, M:; Hermans, A.; Breuer, M.; Grosveld, G.; Berr Oncogene Res. 1, 103-112, 1987
A; Title: Comparison of the human and mouse PIM-1 cDNAs: Nucleotide sequer A; Reference number: 158412; MUID:88217305; PMID:3329709
A; Recession: I58412
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-313 < CDOM>
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TVHUP1

TVHUP1

Protein kinase (EC 2.7.1.37) pim-1 - human

N;Alternate names: kinase-related transforming protein pim-1; pim-1 proto-oncogene

C;Species: Homo sapiens (man)

C;Bate: 31-Mar-1989 #sequence revision 07-Oct-1994 #text_change 09-Jul-2004

C;Accession: JU0327, AdS554; A27476; I58812

R;Reeves, R.; Spies, G.A.; Kiefer, M.; Barr, P.J.; Power, M.

Gene 90, 303-307, 1990

A;Title: Primary structure of the putative human oncogene, pim-1.

A;Reference number: JU0327; MUID:90382681; PMID:2205533

A;Accession: JU0327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 54, 105-111, 1987
A,Title: The cDNA sequence and gene analysis of the human
A,Reference number: A27476, MUID:87277423, PMID:3475233
A,Accession: A27476
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                                 Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonis, Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonis, Superfamily: kinase-related transforming protein; protein kinase homology; Keywords: ATP; autophosphorylation; phosphorycein; phosphotransferase; proto-oncogen; 36-290/Domain: protein kinase homology KIN>;36-290/Domain: protein kinase ATP-binding motif; 44-52/Region: protein kinase ATP-binding motif
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                                                                                                                     TTTGAAGAAATCCGGAACCATCCGTGGATGCAGGGTGACCTCCTGCCCCAGGCAGCTTCT
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97.12%
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Matches:
Conservative:
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294
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260 840 280 720

780

660

220

600

200

120 420 140 480 160

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A;Accession: B43093
A;Molecule type: mcMa
A;Residues: 'M', 61-370 <VA3>
A;Residues: 'M', 61-370 <VA3>
A;Cross-references: GB:L41495; N:
A;Octe: 34K form
C;Comment: Pim-2 autophosphorylat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: Pim-2
A;Map position: X
A;Start codon: CTG

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Query Match:
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A; Residues: 1-370 < VAN>
     문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-705-757-5 (1-942) x S55333 (1-370)
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;Residues: 'M',27-370 <VA2>
;Cross-references: GB:L41495;
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                                                                                                 LeuLeuTrpLysValGlyGluGlyAsnGlyHisProGlyValIleArg
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Matches:
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submitted to the EMBL Data Library, Jr
A;Reference number: Z19538
A;Accession: T22255
A;Status: preliminary; translated from
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:Q20443; EN
A;Experimental source: clone F45H7
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F45H7.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T22255 R;Percy, C.
                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:F45H7.4
A;Map position: 3
A;Introns: 72/3; 160/3;
C;Superfamily: kinase-re
                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
                                                                                                                                   US-10-705-757-5 (1-942)
                                                       ATGCAGGGTGACCTCCTGCCCCAGGCAGCTTCTGAGATCCATCTGCACAGTCTGTCACCG
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628.00
64.15%
46.04%
35.91%
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Matches:
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submitted to the EMBL Data Library, February A, Description: The sequence of C. elegans co A; Reference number: Z18350
A, Accession: T15435
A; Status: preliminary; translated from GB/EM A, Molecule type: DNA A, Residues: 1-409 < FAV A, Cross-references: EMBL: U00034; NID: 9458983 A, Experimental source: strain Bristol N2 C; Genetics: A; Gene: CESP: C06E8.3
A; Introns: 24/1; 76/3; 107/2; 145/3; 199/1;
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Apporthetical protein C06E8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #tc C;Accession: T15435

R;Pavello, A.
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Best Local Similarity:
Query Match:
DB:
protein kinase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996
C;Accession: I49072
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ThrGlyGluValLysLeuValAspPheGlyAlaThrAlaTyrAlaGluLysAlaThrLys
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GlyGlnGlnProValAlaValLysPheValGlnHisLysHisValArgSerTrp---Thr
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Mismatches:
Indels:
Gaps:
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254 774 214 654 594 174 477 134 114 357 94

75 237 56 36

807 283

323

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R;Ruiz, J.C.; Conlon, F.L.; Robertson, E.J.
Mech. Dev. 48, 153-164, 1994
A;Title: Identification of novel protein kinases expressed in tagretarence number: 149071; MUID:95200798; PMID:7893599
A;Refearence number: 149072; MUID:95200798; PMID:7893599
A;Accession: I49072
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-481 <RES-
A;Cross-references: EMBL:U11494; NID:g595420; PIDN:AAA67926.1;
C;Superfamily: protein kinase homology
C;Keywords: ATP
C;Keywords: ATP
F;71-324/Domain: protein kinase homology <KIN-
F;79-87/Region: protein kinase ATP-binding motif
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                                   LysGluTyrGluGlyProGlnLeuAspValTrpSerLeuGlyValValLeuTyrValLeu
                                                                     CATCGCTACCACGCAGGTCGGCAGCTGTCTGGTCCCTTGGGATCCTGCTCTATGACATG
                                                                                                          GluProLeuSerThrCysValGlySerProProTyrAlaAlaProGluValPheGluGly
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T10449
probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
probable serine/threonine-specific protein kinase
(;Species: Cucumis sativus (cucumber)
C;Species: Cucumis sativus (cucumber)
C;Accession: T10449
R;Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z17020
A;Accession: T10449
A;Accession: T10449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-504 <GUM>
A;Cross-references: UNIPROT:P93113; EMBL:Y10036
A;Experimental source: cv. Masterpiece; cotyledon
C;Function: Catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily; AMP-accivated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;6-260/Domain: protein kinase homology <KIN>
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TGCCACAACTGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTG
                                                      ArgLeuGlnGluAspGluAlaArgAsnPhePheGlnGlnIleIleSerGlyValGluTyr
                                                                                       GCCCTACAGGAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCAT
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valvalMetGluTyrValLysSer---GlyGluLeuPheAspTyrIleValGluLysGly
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A; Molecule type: DNA
A; Residues: 1-1101 < ANS>
A; Cross-references: UNIPROT: Q08217;
A; Cross-references: Grain S288C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein YOL045w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2034
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 16-Aug-2004
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                      A;Molecule type: DNA
A;Residues: 1-512 <LEG>
A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:A
A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:A
A;Cross-references: UNIPROT:Q38997; GB:M93023; NID:g166599; PIDN:A
R;Thuemmler; F; Kirchner; M; Teuber; R; Dittrich, P.
Submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22
A;Reference number: S58256
A;Accession: S58266
A;Accession: S58266
A;Accession: S58266
A;Accession: S78266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: preliminary
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID
:CAA60529.1; PIDR:CAA605
                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - N;Alternate names: protein kinase SNF1 homolog (;Specise: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_chan C;Accession: JC1446; SS8266; S66334 R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, Gene 120, 249-254, 1992 A;Title: Structure and expression of a gene from Arabidopsis A;Reference number: JC1446; MUID:93013041; PMID:1339373 A;Accession: JC1446
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A; Title: Differential accumulation of the transcripts
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A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C;Comment: This enzyme plays an important role in a signal transduction cascade regulati
C;Gene: AKin10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3
C;Function:
C;Superiamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted
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                                    IleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAsp---AspGluAsnIleProAsn
                                                                                                                    GluValileSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSerCysGlyVal
                                                                                                                                                        GAGTGGATTCGCTACCATCGCTACCACGGCAGGTCGGCAGCTGTCTGGTCCCTTGGGATC
                                                                                                                                                                                             IleMetArgAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyrAlaAlaPro
                                                                                                                                                                                                                                    CTGCTCAAGGACACAGTCTACACGGACTTTGAT---GGGACCCGAGTGTACAGTCCTCCA
                                                                                                                                                                                                                                                                                                             AACATCTTAATCGACCTGAGCCGCGGCGAAATCAAACTCATCGACTTCGGGTCGGGGCG
                                                                                                                                                                                                                                                                                                                                                    TTTATCACCGAACGAGCCCCTACAGGAGGACCTGGCCCGAGGATTCTTCTGGCAGGTG
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IleLeuArgLeuPheMetHisProHis-----IleIleArgLeuTyrGluValIleGlu
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                                                                             CTGCTCTATGACATGGTCTGCGGAGATATTCCGTTTGAGCACGATGAAGAGATC-----
                                                                                                                                                                                                                                                                          AsnLeuLeuLeuAsp---SerLysCysAsnValLysIleAlaAspPheGlyLeuSerAsn
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21.33%
-ATCAAGGGCCAAGTGTTC---TTCAGGCAAACTGTCTCTTCAGAGTGT
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T13741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1398 <MUR> A;Cross-references: UNIPROT:077268; EMBL:AL031765; l C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, April 1999
A;Description: Sequencing the distal X chromosome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein 2285.8 - fruit fly (Drosophila C;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 C;Accession: T13741
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Best Local Similarity:
Query Match:
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A;Introns: 205/3; 227/1; 322/3; 688/3;
A;Note: EG:22E5.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: Z17668
A; Accession: T13741
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                    ||||:::||| ||||||:::||||:::|||||||:::
| AspLeuLysAlaGluAsnLeuLeuLeuAspLeuAsnMet---AsnIleLysIleAlaAsp
                                                                                                 LysLeuLysGluProMetArgValGlyPheTyrAspIleGluArgThrIleGlyLysGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgAspLeuIleProArgMetLeuValValAspProMetLysArgValThrIleProGlu
                                                           GACATCAAGGACGAGAACATCTTAATCGACCTGAGCCGCGGCGAAATCAAACTCATCGAC
                                                                                                                                                                             GlyGluIlePheAspTyrileAlaLysTyrGlyArgMetSerGluSerAlaAlaArgPhe
                                                                                                                                                                                                                 CAAGACCTCTTCGACTTTATCACCGAACGAGGAGCCCTACAGGAGGACCTGGCCCGAGGA
                                                                                                                                                                                                                                                                                                                                                                          CCCATGGAAGTGGTCCTGTTGAAGAAGGTGAGCTCGGACTTCTCGGGCGTCATTAGACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAGAGAAGGAGCCCCTGGAG---TCGCAGTACCAGGTGGGCCCGCTGTTGGGCAGCGGT
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                                                                                                                          TTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGCCACAACTGCGGGGGTTCTCCACCGC
                                                                                                                                                                                                                                                        TyrGlnValMetGluThrLysAsnMetIleTyrIleValSerGluTyrAlaSerGln---
                                                                                                                                                                                                                                                                                             CTGGACTGGTTCGAGAGGCCCGATAGTTTCGTGCTGATCCTGGAGAGGCCCGAACCGGTG
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Matches:
Conservative:
Mismatches:
Indels:
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PID:e1329905; PIDN:CAA2

185

258 169

318

203

558 262

281

242 438

498

378

222

198

150

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A;Crose-references EMBL:S93805

R;Sidhu, R.S.; Mathewes, S.; Bollon, A.P.

Gene 107, 111-118, 1991

A;Title: Selection of secretory protein-encoding genes by f A;Title: Selection of secretory protein-encoding genes by f A;Reference number: JH0483; MUID:92077420; PMID:1743509

A;Accession: JH0486

A;Molecule type: DNA

A;Residues: 1-72, 'E', 74-154 <SID>
C;Genetics: C;Genetics: FUN31; SSP138

A;Cross-references: SGD:S0000015; MIPS:YAL017w

A;Map position: 1L
C;Superfamily: protein kinase homology
C;Keywords: ATP; glycoprotein; phosphotransferase; serine/t F;1096-1356/Domain: protein kinase homology <KIN>
F;1096-1356/Domain: protein kinase homology <KIN>
F;1096-13128/Binding site: carbohydrate (Asn) (covalent) #status
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$33653

$33653

probable serine/threonine protein kinase (EC 2.7.1.-) - yeast (Ss probable serine/threonine protein YAL002; protein YAL017w; secretory protein YAL019w; Sa6717; Sa6712; JH0486

R;Clark, M.W.; Zhong, W.W.; Keng, T.; Storms, R.K.; Ouellette, B. Yeast 9, 543-549, 193

A;Tilla: The YAL017 gene on the left arm of chromosome I of Sacch A;Reference number: S33653; MUID:93311122; PMID:8322517

A;Reference number: S33653; MUID:93311122; PMID:8322517

A;Reference type: DNA

A;Residues: 1-1358 CLLA

A;Residues: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: DNA
A; Residues: 1-867
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A; Residues: 1-864, 867-1358 < OUE>
A; Residues: 1-864, 867-1358 < OUE>
A; Cross-references: EMBL:LO5146; NID:g171851;
R; Clark, M.W.; Zhong, W.W.; Keng, T.; Storms,
Yeast 8, 133-145, 1992
A; Title: Identification of a Saccharomyces cer
A; Reference number: S22266; MUID:92221890; PMI
A; Accession: S36732
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Superfamily: protein kinase homology superfamily: protein kinase homology (Keywords: ATP, glycoprotein; phosphotransferase; serine/threonine-specific (1096-1356/Domain: protein kinase homology <KIN> (1104-1112/Region: protein kinase ATP-binding motif (1104-1112/Region: protein 
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ProTyrAlaAlaProGluValPheGluGlyLysGlnTyrThrGlyProGluIleAspIle
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                                                                                   SerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAsp---AspGlu
                                                                                                                TCCCTTGGGATCCTGCTCTATGACATGGTCTGCGGAGATATTCCGTTTGAGCACGATGAA
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serine/threonine-specific protein kinase (EC 2.7.1.-)
NyAlternate names: SNF1 protein kinase omolog AKINI1
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #tc
C;Accession: T52633
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A;Title: Regulatory interaction of PRL1 WD protein with Arabidopsis A;Reference number: Z25116; MUID:99238528; PMID:10220464
A;Accession: T52633
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AACATCTTAATCGACCTGAGCCGCGGCGAAATCAAACTCATCGACTTCGGGTCGGGGGCG
                                      CTGGAGGCCGTGCGGCATTGCCACAACTGCGGGGTTCTCCACCGCGACATCAAGGACGAG
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A;RCCGBBACH.

A;Status; preliminary
A;Molecule type: mRNA
A;Rosidues: 1-61,'A',63-513 <HA2>
A;Rosidues: 1-61,'A', 63-513 <HA2
A;Rosidues: 1-61,'A', 63-513 <HA2
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LeuSerAspSerAlaArgAspLeuIleProLysLeuLeuAsnIleAspProMetLysArg
                                                                                                                                                                                                                ValTrpSerCysGlyValValLeuTyrAlaLeuLeuCysGlySerValProPheAspAsp
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                                   CCCTCCTTTGAAGAAATCCGGAACCATCCGTGGATGCAGGGTGACCTC
                                                                                                         GTCTCTTCAGAGTGTCAGCACCTTATTAAATGGTGCCTGTCCCTGAGACCGTCAGATCGG
                                                                                                                                          AspAsnIleProSerLeuPheArgLysIleLysGlyGlyThrTyrIleLeuProSerTyr
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Search completed: September 22, 2005, 17:20:41 Job time: 40.871 secs

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Command line parameters:

-WODEL-frame+ n2p.model -DEV=xlp
-Q-Cgn2 1/USPTO gp.model -DEV=xlp
-Q-cgn2 1/USPTO gp.model -DEV=xlp
-Q-cgn2 1/USPTO gp.model p/US10705757/runat 22092005 115015 22129/app query.fasta 1.5333
-Q-/cgn2 1/USPTO gpool p/US10705757/runat 22092005 115015 22129/app query.fasta 1.5333
-DB=UniProt -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LÖOPCL=0 -LÖOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR GCORE-pot -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=US10705757 @CGN 1 1 980 @runat 22092005 115015 22129 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Delop 6.0 , F
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PIM2_MOUSE
PIM2_HUMAN
                                                                                                                                                                                                 BSDOW TWIN
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6203.583 Million cell updates/sec
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             Q9n0p9
Q9pu85
P58750
070444
Q86v86
Q91822
Q811x8
Q66ii1
Q8r2p0
Q62070
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Q8cfn8
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felis silve
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•	•	•	21.3	•	21.4	21.4	21.5	•	21.6	•	21.6	21.7	21.7	21.7	21.9	•		•	22.8	•	28.8	•		•	48.0	48.1	8	48.5	
1398	1398	794	535	1229	518	292	643	776	1107	779	661	1336	1101	504	432	1206	658	125	1383	134	566	378	441	221	310	310	310	310	
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Q9W532	077268	KI11_HUMAN	KI10_ARATH	Q6CKW4	Q7PR39	Q7QD91	Q7R0B9	SN1L_RAT	Q6C310	SN1L MOUSE	ARK5_HUMAN	Q6FRS7	KOE5 YEAST	P93113	Q7QXR8	Q6FUT1	Q641K5	Q6Q2K5	PASK MOUSE	Q6P2J9	Q17737	Q8T3F1	Q20443	Q8R1Z0	Q6DI52	PIM1 BRARE	JFW	Q7ZVJ5	
	077268 drosophila			kluyveromy		anopheles		rat	yar	mus 1	5 hom	cand	saccharo	cucumis s	3 giardia	cand	m	cani	mus mu		Q17737 caenorhabdi	Q8t3f1 caenorhabdi	caer	0	Q6di52 brachydanio	vı	φ	Q7zvj5 brachydanio	

ALIGNMENTS

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SEQUENCE FROM N.A.

MEDLINE=86272109; PubMed=3015420; DOI=10.1016/0092-8674(86)90886-X;
Selten G., Cuypers H.T., Boelens W., Robanus-Maandag E., Verbeek J.,
Domen J., van Beveren C., Berns A.;
"The primary structure of the putative oncogene pim-1 shows extensive homology with protein kinases.";
Cell 46:603-611(1986).
                                                                                 -!- SUBUNIT: Binds to RP9.

!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity)
-!- PTM: Autophosphorylated (By similarity).
-!- DISEASE: Frequently activated by provirus insertion in murine leukemia virus-induced T-cell lymphomas.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
                                                                                                                                                                                MEDIINE-20389540; PubMed=10931201;
Maita H., Harada Y., Nagakubo D., Kitaura H., Ikeda M., Tamai K.,
Takahashi K., Ariga H., Iguchi-Ariga S.M.M.;
"PAP-1, a novel target protein of phosphorylation by Pim-1 kinase.";
Eur. J. Biochem. 267:5168-5178(2000).
-i- CATALYTIC ACTIVITY; ATP + a protein = ADP + a phosphoprotein.
                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                     (By similarity).
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                         EMBL
                       a collaboration
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homo sapien

restrictions

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Query Match:
DB:
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InterPro; IPRO11009; Prot kinase.
InterPro; IPRO08271; Ser_Thr_pkin_AS.
Pfam; pF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE DOM; I.
PROSITE; PS0011; PROTEIN KINASE ST; I.
PROSITE; PS00108; PROTEIN KINASE_ST; I.
PROSITE; PS00108; PROTEIN KINASE_ST; I.
ATP-binding; Nuclear protein; Phosphorylation; Profession, Protein kinase, Transferase.
Serine/threonine-protein kinase; Transferase.
DOMAIN
Serine/threonine-protein kinase; Transferase.
DOMAIN
BIND
4 52
NP BIND
4 52
NP BIND
67 ATP (By similarity).
BINDING
67 ATP (By similarity).
BINDING
67 ATP (By similarity).
SEQUENCE 313 AA; 35536 MW; 79F4779E9DCBDC16 CI
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PIR; A24169; TVMSP1.
HSSP; Q63450; 1A06.
MGD; MGI:97584; Pim1.
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Proton acceptor (By s:
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Matches:
Conservative:
Mismatches:
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RC STRAIN=6278L/6; TISSUE=Brain, and Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX MEDLINE=22388257; Pebmed=1247932; DOI=10.1073/pnas.242603899;
RX MILLINE=22388257; Pebmed=1247932; DOI=10.1073/pnas.242603899;
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RX MEDLINE=2238827; MEDLINE=24799;
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Q8CFN8;
01-MAR-2003
                                                                                                                      TISSUE=Eye;
Strausberg F
Submitted (J
   Strausberg
Submitted (
                                                                                                                                                                                                                                                                                             "Generation and initial analysis of more and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16
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NCBI_TaxID=10090;
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   g R.;
(JUN-2003)
                                                                                                                                              JR.;
(JAN-2003)
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                                                         .A.
TISSUE=Brain;
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Sciurognathi;
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A Strauberg R.;

L Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

C -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; BC042885; AAH42885.1; -.

R EMBL; BC053019; AAH53019.1; -.

R EMBL; BC053316; AAH5316.1; -.

R EMBL; BC053316; AAH5316.1; -.

R MGD; MG1:97584; Pim1.

DR GO; GO:000524; FinTp binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity:

DR GO; GO:0006469; P:protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R EMBL; BC055316; AAH55316.1; -..

R MGD; MGI:97584; Piml.

R GG; GO:0005524; F:ATP binding; IEA.

R GG; GO:0004674; F:protein serine/threonine kinase activit

R GG; GO:0004674; F:protein amino acid phosphorylation; IEA.

R GG; GO:0006468; P:protein amino acid phosphorylation; IEA

InterPro; IPR011009; Kinase like.

InterPro; IPR000719; Prot kinase.

InterPro; IPR000719; Prot kinase.

InterPro; IPR0002290; Ser_thr_pkin_AS.

R InterPro; IPR000290; Ser_thr_pkin_AS.

R InterPro; IPR008271; Ser_thr_pkin_AS.

R Pfam; PF00069; Pkinase; I.

R PfAm; PF00069; Pkinase; I.

R PFONDIN; SM00120; S TKC; I.

R PROSITE; PS00110; PROTEIN_KINASE_DOM; I.

R PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00109; PKINASE_ST; 1.

R PROSITE; PS00109; ROTEIN_KINASE_ST; 1.

R PROSITE; PS00109; ROTEIN_KINASE_ST; 1.

R PROSITE; PS00110; PROTEIN_KINASE_ST; 1.

R PROSITE; PS00110; PROTEIN_KINASE_ST; 1.
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STRAIN-C57BL/6; TISSUE-Brain;
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Pfam; PF00069; Pkinase; T.

ProDom; PD000001; Prot_kinase; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE T; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Nuclear protein; Phosphorylation; Serine/threonine-protein kinase; Transferase.

DOMAIN

38 290 Protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujino Y., Satoh H., Hisasue M., Masuda K., Ohno K., Tsu
"The cDNA sequence of the feline pim-1 oncogene.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosph
-! SUBCUNIT: Binds to RP9 (By similarity).
-! SUBCULILAR LOCATION: Cytoplasmic and nuclear (By si
-!- PTM: Autophosphorylated (By similarity).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase fa
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entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
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                                                                                                                                                                                                                                                                                     EMBL; AB073748; BAB71752.1;
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IPRO11009; Kinase like.
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IPR008271; Ser thr pkin AS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUB-Testis;
MEDLINE-92319652; PubMed-1620615;
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05-JUJ-2004 (Rel. 44, Last annotation update)
Proto-oncogene serine/threonine-protein kinase
Name=Pim1; Synonyms=Pim-1;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRODOM; PD000001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE DOM; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Nuclear protein; Phosphorylation;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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IPR011009; Kinase like.
IPR000719; Prot kinase.
IPR008271; Ser thr pkin As.
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RESULT 5
PIM1 HUMAN STANDARD; PRT; 313 AA.

ID PIM1 HUMAN STANDARD; PRT; 313 AA.

AC P1309; Q96RG3;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JAN-1990 (Rel. 21, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Proto-oncogene serine/threonine-protein kinase Pimane-PIM1;
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebration
OC Mammalia; Eutheria; Primates; Catarrhini; Hominida
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RC TISSUB=Kidney;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA MISSUBSETR R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Brownstein M.J., Usdin T.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rodrigue K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Halkesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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Gene 54:105-111(1987).
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MEDLINE=88217305; Publ
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a H., Iguchi-Ariga S.M.M.;
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R GO; GO:0005737; C:cytoplasm; TAS.

R GO; GO:0004574; P:protein serine/threonine kinase activity; TAS.

R GO; GO:0004674; P:protein amino acid phosphorylation; TAS.

R GO; GO:0007275; P:development; TAS.

R GO; GO:0006468; P:protein amino acid phosphorylation; TAS.

R Interpro; IPR001109; Kinase: like:

R Interpro; IPR008771; Ser Chr.pkin_AS.

R Interpro; IPR008771; Ser Chr.pkin_AS.

R FAGN: PF00069; Pkinase; I.

R PROSITE; PF00069; Pkinase; I.

R PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

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Johnson T., Lilly M.B., Kraft A.S.;

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EMBL; AF386792; AAK70871.1; -.
EIRBL; JU0327; TVHUP1.
Genew; HGNC:8986; PIM1.
H-INVDB; HIX0005835; -.
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EMBL; M54915; AAA36447.1; -.
EMBL; M24779; AAA81553.1; -.
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Serine/threonine-protein kinase; Transferase.
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Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE ST; 1.
ATP-binding; Nuclear protein; Phosphorylation; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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Conservative:
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RESULT
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Q9PU85;
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MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;

MEDLINE=20180111; PubMed=10713710; DOI=10.1038/sj.onc.1203355;

Bichmann A., Yuan L., Breant C., Alitalo K., Koskinen P.J.;

"Developmental expression of Pim kinases suggests functions all outside of the hematopoletic system.";

Oncogene 19:1215-1224(2000).

-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprote:
                                                                                                                                                                                           Name=PIM3; Synonyms=PIM-3;
Coturnix coturnix japonica (Japanese
Eukaryota; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                     28-FEB 2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
05-JUL-2004 (Rel. 44, Last annotation
Serine/threenine-protein kinase Pim-3
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PTM: Autophosphorylated SIMILARITY: Belongs to
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 kinase
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SMART; SM00220; S.TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Phosphorylation; Serine/threonine-protein
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InterPro; IPR011009; Kinase like.
InterPro; IPR001719; Prot kinase.
InterPro; IPR002790; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
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TyrG1yCysG1yValValHisArgAspIleLysAspGluAsnLeuLeuValAspLeuArg
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RC STRAIN=FVB/N; TISSUE-Colon, and Salivary gland;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE-2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RX Allausner R.D., Collins F.S., Rang G.M., Rubin G.M., Hong L.,

RX Allausner R.D., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RX Allausner R.D., Collins R.S., Farmer A.A., Rubin G.M., Hong L.,

RX Allausner R.D., Collins R.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RX Allausner R.D., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J.,

RX Allausner R.D., Wolley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J.,

RX Allausner R.D., Wolley R.C., Shevchank K.J., Malek J.A., Gunaratne P.H.,

RX Allausner R.D., Wolley R.C., Shevchank R.J., Gibbs R.A.,

RX Allausner R.D., Wolley R.C., Shevchank R.J., Marta M.A.,

RX Allausner R.D., Voung A.C., Shevchank V., Bouffard G.G.,

RX RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

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RX RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RX RA Rodriguez A.C., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human for the following for the Schwarz A.
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This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI TaxID=10090;
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roton acceptor (By similarity).
DD68CBF46354851E CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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MEDLINE=98298176; PubMed=9632723; DOI=0.1074/jbc.273.26.16535;

A Peldman J.D., Vician L., Crispino M., Tocco G., Marcheselli V.L.,

A Bazan N.G., Baudry M., Herschman H.R.;

"KID-1, a protein kinase induced by depolarization in brain.";

J. Biol. Chem. 273:16535-16543(1998).

C -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

C -!- TISSUE SPECIFICITY: Present in a number of unstimulated tissues

C -!- INDUCTION: By membrane depolarization or forskolin.

C -!- PTM: Autophosphorylated.

C -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM

n:hfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FBB-2003 (Rel. 41, Last sequence upda 05-JUL-2004 (Rel. 44, Last annotation up Serine/threonine-protein kinase Pim-3 (E Kid-1) (Kinase induced by depolarization Name-pim3; Synonyms-Kid1; Rattus norvegicus (Rat).

Bukaryota; Metazoa; Chordata; Craniata; Mammalia; Butheria; Rodentia; Sciurognat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIM3 RAT
070444;
28-FEB-2003
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                         EMBL; AF086624; AAC68900.1;
EMBL; AF057026; AAC36065.1;
HSSP; Q03656; 1HOW.
RGD; 620462; Pim3.
                                                                                                                                                                                                                                                                                                                                                                                                      Konietzko U., Kuhl D.; "Pim-3 is a member of the possibilitied (AUG-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
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IPR000719; Prot kinase.
IPR008271; Ser_thr_pkin_AS
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he EMBL/GenBank/DDBJ
                                                                   ALT_INIT.
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ACT_SITE
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SMART; SM00220; S TKC; 1.

PROSITE; PS0010; PROTEIN KINASE ATP; 1.

PROSITE; PS0011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
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                                                                                                                                                             ATCACCGAACGAGGAGCCCTACAGGAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTG
                                                                                                                                                                                   ProAspGlyPheLeuLeuValLeuGluArgProGluProAlaGlnAspLeuPheAspPhe
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         ATTCGCTACCATCGCTACCACGGCAGGTCGGCAGCTGTCTGGTCCCCTTGGGATCCTGCTC
                                                                         LeuLeuValAspLeuArgSerGlyGluLeuLysLeuIleAspPheGlySerGlyAlaVal
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ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity).
DD6C9BF4635F851E CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

R. Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

R. Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Altechenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

R. Altechenko L., Mozusina K.J., Toshiyuki S., Carninci P., Prange C.,

R. Altechenko L., Mozusina N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R. Boeak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

R. Altechenko J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R. Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

R. Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez B.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez B.C., Grimwood J., Schmutz J., Myers R.M.,

R. Rodriguez B.C., Grimwood J., Schmutz J., Myers R.M.,

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29-MAR-2004 (Rel. 43, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase Pim-3 (EC 2.7.1.37).
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                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION FROM ESTS.

MEDLINE=22682943; PubMed=12798037; DOI=10.1016/S1476-9271(02)00095-6; Chichester C., Nikitin F., Ravarini J.-C., Lisacek F.; Chichester C., Nikitin F., Ravarini protein forms."; "Consistency checks for characterizing protein forms."; Comput. Biol. Chem. 27:29-35(2003).

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-i- SIMILARITY: Belongs to the Ser/Thr protein kinase family. PIM
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                                          EMBL; BC052239; AAH52239.1; ALT_INIT.
InterPro; IPR0011009; Kinase_like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
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PSS0011;
PS00108;
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                                                                                          CTCAAGGACACAGTCTACACGGACTTTGATGGGACCCGAGTGTACAGTCCTCCAGAGTGG
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0011; PROTEIN_KINASE_DOM; 1.
0108; PROTEIN KINASE_ST; 1.
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ATP (By similarity).
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PING XENLA STANDARD; PRT; 323

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DY 15-DEC-1998 (Rel. 37, Last sequence updat of the protein kinase pin-3 (Region of the sequence)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PHOSPHORYLATION SITES.
MEDLINE=97256766; PubMed=9099695; DOI=10.1074/jbc.272.16.10514;
Palaty C.K., Kalmar G., Tai G., Oh S., Amankawa L., Affolter M. Aebersold R., Pelech S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=PiM3; Synonyms=PIM1;
Xenopus laevis (African clawed frog),
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of the autophosphorylation sites of the Xenopus laevis pim-1 proto-oncogene-encoded protein kinase.";
J. Biol. Chem. 272:10514-10521(1997).
-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAC-----GCCACCAAGCTGGCGCCGGGCAAA---GAGAAGGAGCCCCTGGAGTCGCAG
                                                                                                                                                                                                                                                                                                                                       IleValMetGluArgProGluProValLysAspLeuPheAspTyrIleThrGluLysGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisLeuProValLysIleLeuGlnProValLysValAspLysGluProPheGluLysVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerGluAspCysAspLeuArgLeuArgThrIleAspAsnAspSerSer
                                          CAGGCAGCTTCTGAGATCCATCTGCACAGTCTGTCACCGGGATCCAGC
                                                                 AGCCGCGGCGAAATCAAACTCATCGACTTCGGGTCGGGGGGGCGCTGCTCAAGGACACAGTC
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80.38%
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63.64%
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Conservative:
Mismatches:
Indels:
Gaps:
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R GO; GO:0005524; F:Arm.

R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

R GO; GO:0016740; F:transferase activity; IEA.

R GO; GO:0016468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR011099; Kinase; like.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR000719; Prot kinase.

R InterPro; IPR00071; Prot kinase; 1.

R Pfam; PF00069; Pkinase; I.

R Pfam; PF000001; Prot kinase; 1.

R PFCDOm; PD0010001; Prot kinase; 1.

R PROSITE; PS00107; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.

R PROSITE; PS00108; PROTEIN KINASE T; 1.

R PROSITE; PS00108; PROTEIN KINASE DOM; 1.
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Q811X8;
01-JUN-2003
01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KID1.
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                                                                                              TCCGATTGGGGAGAACTGCCCAATGGCACCCGAGTGCCCATGGAAGTGGTCCTGTTGAAG
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ThrGluTTpGlySerLeu---GlyGlyValAlaValProLeuGluValValLeuLeuArg
                                                                                                                                            CCCGATAGTTTCGTGCTGATCCTGGAGAGGCCCGAACCGGTGCAAGACCTCTTCGACTTT
                                                                                                                                                                                                                                     GlyValAspHisLeuProValLysIleLeuGlnProAlaLysAlaAspLysGluSerPhe
        -----AACGACCTGCACGCCACCAAGCTGGCGCCAAA---GAGAAGGAGCCCCTG
                                                                                                                                                                                                                                                                                                                               (1-942)
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.yAlaAlaGlyGlyAlaArgGlyValIleA
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1110.00
81.33%
70.67%
63.46%
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                                                    24,
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Last sequence update)
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Matches:
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                                                                                                               A PubMed-12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
Generation and Initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q66III; PRELIMINARY; PRT; 318 AA.
Q66III; PRT; 318 AA.
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.

Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-Embryo;
    TISSUE=Embryo;
Klein S., Gerh
                                            SEQUENCE FROM N.A.
                                                                                                  mouse cDNA sequences."
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      Gerhard D.S.;
                                                                                 Acad. Sci.
                                                                                    U.S.A.
                                                                                 99:16899-16903 (2002)
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Best Local Similarity:
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ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nterPro;
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srPro; IPR011009; Kinase like.
erPro; IPR000719; Prot kinase.
erPro; IPR0002290; Ser thr pkinase.
erPro; IPR008271; Ser thr pkin AS.
erPro; IPR001245; Tyr pkinase.
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                                                                                            ACGGACTTTGATGGGACCCGAGTGTACAGTCCTCCAGAGTGGATTCGCTACCATCGCTAC
                                                                                                                                          ThrAlaGluLeuLysLeuIleAspPheGlySerGlyAlaLeuLeuArgAspAlaValTyr
                                                                                                                                                                 CGCGGCGAAATCAAACTCATCGACTTCGGGTCGGGGGGGCTGCTCAAGGACACAGTCTAC
                                                                                                                                                                                                                                                                                                      CTACAGGAGGACCTGGCCCGAGGATTCTTCTGGCAGGTGCTGGAGGCCGTGCGGCATTGC
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Stapleton M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Bosak S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Blakes S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Marra M.A., I
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01-OCT-2003
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=723822382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=7238222382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=7238222382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=7238222382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=7238222382257; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; DOI=10.1073/pnas.24260389;
MEDLINE=72382257; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; DOI=10.1073/pnas.242603899;
MEDLINE=72382257; DOI=10.1073/pnas.24267; DOI=10.1073/pnas.24267;
MEDLINE=72382257; DOI=10.1073/pnas.24267; DOI=10.1073/pnas.24267; DOI=10
  Pfam; PF00069; Pkinase; I.

ProDom; PD00001; Prot kinase; 1.

SMART; SM00220; STKc; I.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE TOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 311 AA; 34486 MW; F7B770908D23A710 CRC64;
                                                                                                                                                                    -i- SIMILARITY: Belongs to the Ser/Thr protein kinase family BMBL; BC027376; AAR27376.1; -.
GMBL; BC027376; AAR27376.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity;
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:00166468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR0109; Kinase ike.
InterPro; IPR000719; Prot_kInase.
InterPro; IPR0002790; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
Fiam; PF00069; Pkinase; I.
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STRAIN=FVB/N; TISSUE=Mammary tumor.
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"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A.
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(APR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                           MetGlnSer--
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AsnArgValLeuGlyTrpSerThrValSerAspSerValThrCysProLeuGluValAla
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                                             ATGCAGGGTGACCTCCTGCCCCAGGCAGCTTCTGAGATCCATCTGCACAGTCTGTCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTTGAAGAAGGTG-----AGCTCGGACTTCTCGGGCGTCATTAGACTTCTGGACTGG
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                                                                                             CysLeuAlaProLysProCysSerArgProSerLeuGl
                                                                                                                                          TGCCTGTCCCTGAGACCGTCAGATCGGCCCTCCTTTGAAGAAATCCGGAACCATCCGTGG
                                                                                                                                                                                          GluAlaGluLeuHisPheProAlaHisValSerProAspCysCysAlaLeuIleArgArg
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    ProAlaGluGluLysProIleAsnSerSerLysGlySerPro

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Alignment Scores:
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REMBL; L41495; AAA98923.1; -.

REMBL; L41495; AAA98924.1; -.

REMBL; L41495; AAA98923.1; -.

REMBL; L41495; AAA9893.1; -.

REMBL; L41495; AAA9893.1; -.

REMBL; L4149, AAA9893.1; -.

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van der Lugt N.M., Domen J., Verhoeven E., Linders K.,
van der Gulden H., Allen J., Berns A.;
"Proviral tagging in 8 mu-myc transgenic mice lacking
oncogene leads to compensatory activation of Pim-2.";
EMBO J. 14.2536-2544(1995).
-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Pim2; Synonyms=Pim-2;
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                         Serine/threonine-protein CHAIN 1 370
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ATP (By similarity).
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                                             TGCCTGTCCCTGAGACCGTCAGATCGGCCCTCCTTTGAAGAAATCCGGAACCATCCGTGG
                                                                                            GluAlaGluLeuHisPheProAlaHisValSerProAspCysCysAlaLeuIleArgArg
                                                                                                                      AAGGGCCAAGTGTTCTTCAGGCAAACTGTCTCTTCAGAGTGTCAGCACCTTATTAAATGG
                                                                                                                                                                                             ProGluTrpIleSerArgHisGlnTyrHisAlaLeuProAlaThrValTrpSerLeuGly
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-MODEL-frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USFTO_spoel_p/US10705757/runat_22092005_115016_22174/app_query.fasta_1.5333
-Q=/cgn2 1/USFTO_spoel_p/US10705757/runat_22092005_115016_22174/app_query.fasta_1.5333
-DB=PublIshed_ApplicatIons_AA -QFMT=fastan -SUFFIX=-12p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US10705757 @CGN 1 1 743 @runat 22092005_115016_22174
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: /cgn2_6/ptcdata/2/pubpaa/US07_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep.*
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_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 US-09-971-791-7

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Sequence 7, Application US/09971791
Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Kyle MacBetth
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 35800/238856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 313
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; ORGANISM: Mus
US-09-971-791-7
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Percent Similarity:
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; SEQ ID NO 14
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-348-081-14
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APPLICANT: MUELLER, Guenter
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR
FILE REFERENCE: DEAVZ002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
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US-10-348-081-14
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                   CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuSerArgGly
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RESULT 3
US-10-664-421-2
US-10-664-421-2
Sequence 2, Application US/10664421
Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BREMER, RYAN
APPLICANT: IBRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
                                                                                                                                                                                                                                                                                               SOFTWARE: PATENTIN Ver. 3
SEQ ID NO 2
LENGTH: 313
TYPE: PRT
ORGANISM: Mus musculus
US-10-664-421-2
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBORN, MICHAEL V.
APPLICANT: MILBORN, MICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/411,398
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
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Sequence 10, Application US/10377268

Publication No. US20040171062A1

GENERAL INFORMATION:
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: HIRTH, KLAUS-PETER
APPLICANT: MILBURN, MICHAEL VANCE
TITLE OF INVENTION: METHOD FOR THE DESIGN OF MOLECULAR SCAFFOLDS AND LIGANDS
FILE REFERENCE: 039363/0303

CURRENT APPLICATION NUMBER: US/10/377,268

CURRENT APPLICATION NUMBER: 60/437,929
PRIOR APPLICATION NUMBER: 60/437,929
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR APPLICATION NUMBER: 60/360,651
PRIOR FILING DATE: 2002-02-28

PRIOR PILING DATE: 2002-09-16

PRIOR APPLICATION NUMBER: 60/411,398
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
PRIOR APPLICATION NUMBER: 60/412,341
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; SOFTWARE: PatentIn Ver. 2;
SEQ ID NO 10
; LENGTH: 313
; TYPE: PRT
; ORGANISM: MUS mUSCUlus
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Sequence 6, Application US/10705757

| Publication No. US20040146942A1
| GENERAL INFORMATION:
| APPLICANT: GRUENENTHAL GMBH
| TITLE OF INVENTION: SCREENING METHOD USING PIN
| FILE REFERENCE: 029310.52818US
| CURRENT APPLICATION NUMBER: US/10/705,757
| CURRENT FILING DATE: 2003-11-12
| PRIOR APPLICATION NUMBER: PCT/EP02/05234
| PRIOR APPLICATION NUMBER: DE 101 23 055.9
| PRIOR FILING DATE: 2001-05-11
| NUMBER OF SEQ ID NOS: 11
| SOFTWARE: PATEMARE: PATE
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APPLICANT: BREMER, RYAN B.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: HURT, CLARRENCE R.
APPLICANT: IBRAHIM, PRABHA L.
APPLICANT: IBRAHIM, PRABHA L.
APPLICANT: IBRAHIM, PRABHA L.
APPLICANT: OCKERMAN, REBECCA L.
TITLE OP INVENTION: MOLECULAR SCAPFOLDS FOR PILE REFERENCE: 039363-1702
CURRENT APPLICATION NUMBER: US/10/941,635
CURRENT APPLICATION NUMBER: 60/503,277
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTMARE: PATENTIN Ver. 3.2
SEQ ID NO 2
LENGTH: 313
TYPE: PAT
ORGANISM: Mus musculus
US-10-941-635-2
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Sequence 8, Application US/09971791

Patent No. US20020115120A1

GENERAL INFORMATION:
APPLICANT: ROBERTA Rudolph-Owen
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBeth
ITILE OF INVENTION: MOVEL MOLECULES OF THE H
FILE REFERENCE: 35800/238856

CURRENT APPLICATION NUMBER: US/09/971,791

CURRENT TILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR FILING DATE: 2000-08-23

PRIOR APPLICATION NUMBER: 09/237,543
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; PRIOR FILING DATE: 1999-01-26
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Ve
; SEQ ID NO 8
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-971-791-8
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Sequence 12, Application US/10348081

Publication No. US20040038246A1

GENERAL INFORMATION:

APPLICANT: KORN, MARCUS

APPLICANT: KORN, MARCUS

APPLICANT: SCHANK, Georg

TITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR TYPE 2 DIABETES MELLITUS

FILE REFERENCE: DEAV2002/0004 US NP

CURRENT APPLICATION NUMBER: US/10/348,081

CURRENT FILING DATE: 2003-01-21

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin version 3.2

SEQ ID NO 12

LENGTH: 313

TYPE: DET
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Best Local Similarity:
Query Match:
DB:
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; ORGANISM: Rattus
US-10-348-081-12
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APPLICANT: GRUENTHAL GMBH
TITLE OP INVENTION: SCREENING METHOD USING PI
FILE REFERENCE: 029310.5201080
CURRENT APPLICATION NUMBER: US/10/705,757
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: PCT/EP02/05234
PRIOR FILING DATE: 2002-05-13
PRIOR FILING DATE: 2002-05-13
PRIOR PILING DATE: 2001-05-11
NUMBER OF SED ID NOS: 11
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; ORGANISM: Rattus
US-10-705-757-4
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GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Kyle MacBeth
TITLE OF INVENTION: MOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES '
FILE REFERENCE: 35800/23856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT APPLICATION NUMBER: U01-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR PILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 18, Application US/10081119
Publication No. US20030045491A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TIK in Diagnosis and as
TITLE OF INVENTION: Target in Cancer
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/081,119
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 313
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Sequence 52, Application US/10394322A
Publication No. US20030232391A1
GENERAL INFORMATION:
APPLICANT: SUNESIS PHARMACEUTICALS, INC.
APPLICANT: PRESCOTT, John C.
ITILE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
FILE REFERENCE: 39750-0066 US/10/394,322A
CURRENT APPLICATION NUMBER: US/10/394,322A
CURRENT APPLICATION NUMBER: US/0/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR APPLICATION NUMBER: US 60/366,892
PRIOR FILING DATE: 2003-03-21
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NOS 52
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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APPLICANT: KORN, MARCUS
APPLICANT: MURLLER, Guenter
APPLICANT: MURLLER, Rudolf
APPLICANT: SCHNEIDER, Rudolf
APPLICANT: TSCHANK, Georg
ITITLE OF INVENTION: PIM-3 KINASE AS A TARGET FOR
FILE REFERENCE: DEAVZ002/0004 US NP
CURRENT APPLICATION NUMBER: US/10/348,081
CURRENT FILING DATE: 2003-01-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-10-348-081-13
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US-10-348-081-13
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Publication No. US20040038246A1
                                                                                                                                                        GENERAL INFORMATION
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Publication No. US20040142864A1

Publication No. US20040142864A1

APPLICANT: INFORMATION:

APPLICANT: IBRAHIM, PRABHA

APPLICANT: KUMAR, ABHINAV

APPLICANT: MILBURN, MICHAEL V.

TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE

FILE REFERENCE: 039363/0703

CURRENT APPLICATION NUMBER: US/10/664,421

CURRENT APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR APPLICATION NUMBER: 60/411,398

PRIOR FILLING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOFTMARE: PATENTIN VET: 3.2

SEQ ID NO 1

LENGTH: 313

TYPE: DET
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ORGANISM: Homo
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US-10-664-421-150

Sequence 150, Application US/10664421

Publication No. US20040142864A1

Publication No. US20040142864A1

APPLICANT: IRRAHIM, PRABHA
APPLICANT: IRRAHIM, PRABHA
APPLICANT: KUMAR, ABHINAV
APPLICANT: MILBURN, MICHAEL V.

TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703

CUURENT APPLICATION NUMBER: US/10/664,421

CURRENT FILING DATE: 2003-09-16

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR APPLICATION NUMBER: 60/412,341

PRIOR FILING DATE: 2002-09-20

PRIOR FILING DATE: 2002-09-16

PRIOR FILING DATE: 2002-09-16

NUMBER OF SEQ ID NOS: 169

SOFTWARE: PACENTIN VEY: 3.2

LENGTH: 313

TYPE: PAT
ORGANISM: Homo sapiens

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GluIleHisLeuHisSerLeuSerProGlyProSerLys
     GAGATCCATCTGCACAGTCTGTCACCGGGATCCAGCAAG 939
                      PheGluGluIleGlnAsnHisProTrpMetGlnAspValLeuLeuProGlnGluThrAla
                                 TTTGAAGAAATCCGGAACCATCCGTGGATGCAGGTGACCTCCTGCCCCAGGCAGCTTCT
                                           GAAATCAAACTCATCGACTTCGGGTCGGGGGGCGCTGCTCAAGGACACAGTCTACACGGAC
                                                                                                                                                           CysGlyValLeuHisArgAspIleLysAspGluAsnIleLeuIleAspLeuAsnArgGly
                                                                                                                                                                  TGCGGGGTTCTCCACCGCGACATCAAGGACGAGAACATCTTAATCGACCTGAGCCGCGC
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